June 27-28

Venue

-United Medical Back Building, 16F Lecture Hall, Taipei Medical University

Organized by

-Taipei Medical University -Taipei Professor Jung-Yaw Lin Academic Education Foundation

Supported by

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Ministry of Education
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Introduction of Biomedical Technology and Device Research Laboratories, Industrial Technology Research Institute
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ScreenJCell 從血液中分離、計數以及取得活循環腫瘤細胞的 最佳工具: Circulating Tumor Cells Isolation Kit 監測癌症-就像抽血檢驗一樣簡單!!!



- 最適合 Tumor Sphere forming CSC populations 的 生長與選殖。
- 已有多種來源的癌症幹細胞經過測試可於 Cancer Stem Premium™ medium 中生長並形成 Tumorspheres。
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癌症幹細胞分選套組



自腫瘤細胞及組織中鑑別與分離出腫瘤幹細胞,可以提供非常有價值的細胞分布情形,用以研究癌症幹細胞的起源,以及相較於正常細胞,癌症幹細胞形成、維持與分子變異的機制。 我們的癌症幹細胞,如胞分離試劑盒提供了對分離特定細胞的完美方法。

Markers	Purity of recovered
CD24-/low CD44+	90%-99%
CD24	90%-99%
CD44	90%-99%
CD133	97%-99%
CD326 Epcam	Up to 80%



富利瀚生物科技有限公司 FoliBio Technology Co., Ltd. 產品諮詢專線((

2014 國際癌症新知研討會、第11 屆前瞻生物醫學科學新知研討會 暨第13 屆海峽兩岸生物醫學研討會

> Jun. 27~28, 2014 Taipei Medical University Taipei, Taiwan

Organized by

Taipei Medical University Taipei Professor Jung-Yaw Lin Academic Education Foundation

Supported by

Ministry of Science and Technology Ministry of Education Ministry of Foreign Affairs Ministry of Health and Welfare Introduction of Biomedical Technology and Device Research Laboratories, Industrial Technology Research Institute Institute of Biological Chemistry, Academia Sinica Department of Health, Taipei City Government Department of Information and Tourism, Taipei City Government Office of Research and Development, Taipei Medical University Core Facility Center, Taipei Medical University





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Taipei Medical University (TMU)

Taipei Medical University (TMU), formerly known as Taipei Medical College (TMC), was founded on June 1, 1960 by Dr. Shui-Wang Hu, Dr. Cheng-Tien Hsu and other medical professionals and devoted educators. TMU is located on Wuxing Street in eastern Taipei.

Most of more than 30,000 TMU graduates serve in medical institutions and clinics, while



many others are prominent figures in the fields of research, politics, and business. TMU has 7 colleges, 12 undergraduate schools and 14 graduate institutes as well as three affiliated hospitals - TMU Hospital, Wan Fang Hospital, and Shuangho Hospital. With approximately 3,000 beds, TMU is one of the largest health care systems and offers top-quality teaching, research and clinical services in the Taipei metropolitan area. We work continuously to improve the quality of teaching, research and clinical services with the goal of becoming a fully internationalized university that ranks in the top tier worldwide.

Taipei Medical University Hospital

Taipei Medical University Hospital (TMUH) has been serving Taipei for thirty years. Conveniently located near Taiwan's landmark Taipei 101 tower, TMUH offers a warm atmosphere and friendly environment as well as world-tier medical equipment, top-quality medical personnel and patient-centered service.



The mission of TMUH encompasses education, research and service through innovation, excellence and commitment to life.

We provide our international friends the same high-quality, efficient and accessible medical services. Our steps toward becoming an internationalized medical center include overseas emergency medical transportation, educational exchanges and medical missions. In addition, we help expatriates in Taiwan with quick and convenient medical services and provide assistance for overseas medical activities, collaborating with the government in expanding medical diplomacy as well as setting up a global network of medical contacts.





Taipei Medical University Wan Fang Hospital

Wan Fang Medical Center dedicated to serving the surrounding area, and is committed to community health promotion. Built in 1989, the Wan-Fang Hospital is the first hospital owned by Taipei City government while run by civilians. In 1998, it passed the Regional Hospital Accreditation and was awarded the international quality



certificate of ISO-9002. In 2006, it was awarded the Joint Commission International (JCI) Accreditation. It is the Affiliate Hospital of Taipei Medical University and includes 42 integrated departments of medicine.

Taipei Medical University Shuang Ho Hospital

Shuang Ho Hospital opened on July 1, 2008, with 1580 beds. It is the largest hospital in Taipei County, but also forms a medical "golden triangle" with the Taipei Medical University Hospital and Wan Fang Medical Center, giving a total capacity of over 3000 beds.

Shuang Ho Hospital focuses on providing emergency and critical care, as it is responsible



for first response for Taipei County as the only hospital with a medical helicopter and landing pad. Shuang Ho also has the largest dentistry department, with general and family dentistry and six additional specialized clinics. The hospital has the nation's first disabled patient oral health care center to serve the more than 130,000 disabled people in Taipei County. The Kidney Dialysis Center's method of isolating beds, equipment and sections leads the nation in reducing hepatitis C infection. The hospital plans further expansion in the areas of cancer treatment, neurology, minimally invasive surgery, optometry and vision science, health management, cardiology, rehabilitation, trauma surgery and international medical care.

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Dear colleagues and friends,

On behalf of Taipei Medical University (TMU), we are delighted to welcome you to participate in the coming joint conference of "2014 International Symposium for Recent Advances in Cancer (ISRAC), The 11th Symposium of the Frontiers of Biomedical Sciences and 13th Cross-Strait Symposium on Biomedical Research" which will be held on June 27-28, 2014 at Taipei Medical University (TMU), Taipei, Taiwan. The conference will be a forum for cancer researchers from universities and research institutes around the world to exchange and discuss their recent discoveries and most updated scientific information. There will be five themes for this conference, including Chromosome Instability in Cancer Development, Niche Environment in Cancer Development, Biomarker and Individualized Therapy in Cancer, Stem Cell Research in Cancer, and Translational Medicine in Cancer.

We would like to express our sincere thanks to all, and poster presenters to share with us the recent progress of their research and medical applications in this fast growing field of cancer research at this meeting. I hope that the work presented at this meeting will bring you recent advances in cancer research and medicine, and that each one of you will find the lectures at this meeting useful to your future research. At last, we would like to thank the sponsors, organizing committee members, and volunteers of this meeting for their valuable contributions to this workshop. We hope that your experience at this conference is valuable and memorable.

Thank you again for your participation, and we look forward to seeing you in Taipei Medical University.

Yours sincerely,



Jung-Yaw Lin, Ph. D. Chair. 2014 ISRAC Conference Committee **Emeritus Professor** Department of Biochemistry National Taiwan University Taipei, Taiwan



Wen-Chang Chang, Ph. D. Co-Chair. 2014 ISRAC Conference Committee Academician, Academia Sinica Academician, Academia Sinica **Distinguished Professor** Graduate Institute of Medical Sciences Taipei Medical University Taipei, Taiwan



Yun Yen, MD. Ph. D. Local Organizer, 2014 ISRAC Conference Committee President and Distinguished Professor Taipei Medical University Taipei, Taiwan





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4





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Schedule at a Glance

6/27 Day 1 (F	Pri.)	
08:30~16:40	Registration	16F
09:00~09:15	Opening Remarks	16F
	Conference President Jung-Yaw Lin, Ph.D. (林榮耀院士)	
	Conference Co-President Wen-Chang Chang, Ph.D. (張文昌院士)	
	Conference Local Organizer Yun Yen, M.D., Ph.D. (閻雲校長)	
	Session I: Chromosome Instability in Cancer Development (I)	16F
	Moderator: <u>Yun Yen, M.D., Ph.D. (閻雲校長)</u>	
	Distinguished Professor and President, Taipei Medical University, Taiwan	
09:15~09:45	Edward J. Benz, Jr., M.D.	
	Toward high precision cancer medicine: lessons learned	
	President and CEO. Dana Farber Cancer Institute: Professor. Department of Medicine.	
	Harvard Medical School, USA	
09:45~10:15	JoAnne Stubbe, Ph.D.	
	Radicals your life is in their hands: ribonucleotide reductases as a	
	paradigm	
	Academician, United States National Academy of Sciences Professor, Department of Chemistry, Massachusetts Institute of Technology, USA	
10:15~10:35	Coffee Break	16F/B1
10.10 10.000	Moderator: Wen-Chang Chang. Ph.D. (張文昌院士)	101/21
	Academician, Academia Sinica, Taiwan	
	Distinguished Professor, Graduate Institute of Medical Sciences,	
10.25 11.05	Taipei Medical University, Taiwan	
10:35~11:05	wen-Hwa Lee, Pn.D. (李文華院士)	
	Academician Academia Sinica Taiwan	
	Professor and President, China Medical University, Taiwan	
11:05~11:35	Ying Huang, Ph.D. (黃旲研究員)	
	Structural studies of Rhino protein in piRNA biogenesis	
	Professor, Shanghai Institute of Biochemisrty and Cell Biology,	
11.25 12.05	Chinese Academy of Sciences, China	
11:55~12:05	Jingyi Hui, Pn.D. (思靜叙研究員)	
	The RNA-binding protein QKI suppresses lung cancer-associated	
	Professor Shanghai Institute of Riochemisrty and Cell Riology	
	Chinese Academy of Sciences, China	
12.05~12.15	Group Photography	1 F
12.05, 12.15	Outdoor Plaza	
12:15~13:50	Lunch/ Poster Presentation	4F/B1
	Session II: Cancer Metabolism and Signaling	16F
	Moderator: <u>Andrew HJ. Wang, Ph.D. (王惠鈞院士)</u>	
	Academician, Academia Sinica, Taiwan Distinguished Research Fellow, Institute of Biological Chemistry	
	Academia Sinica, Taiwan	
13:50~14:20	Anning Lin, M.D., Ph.D. (林安寧教授)	
	Computational modeling of IKK signaling	
	Professor and Director, Shanghai Institute of Biochemisrty and Cell Biology,	
	Chinese Academy of Sciences, China	



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14:20~14:50	Hsing-Jien Kung, Ph.D. (龔行健院士)	
	Metabolism and cancer therapeutics: targeting arginine addiction of	
	cancers	
	Academician, Academia Sinica, Taiwan President and Distinguished Investigator, National Health Research Institute, Taiwan	
	Tresident and Distinguished Investigator, National Health Research Institute, Tatwan Moderator: Wan-Wan Lin Ph D (林璐瑜所長)	
	Professor and Director Graduate Institute of Medical Sciences	
	Taipei Medical University, Taiwan	
14:50~15:20	Stephen B. Gruber, M.D, Ph.D., MPH.	
	Molecular pathways and survival in colorectal cancer	
	Director, Norris Comprehensive Cancer Center, University of Southern California, USA	
15:20~15:50	Eva YH. P. Lee, Ph.D. (潘玉華院士)	
	Genetic and hormonal contribution in breast cancer: tissue-specific	
	tumor suppression by BRCA1	
	Academician, Academia Sinica, Taiwan Buofesson, Basis Soimes Dinaston, Dont, of Biological Chemistry	
	& Dept. of Developmental and Cell Biology University of California Irvine USA	
15:50~16:10	Coffee Break	16F/B1
	Session III: Biomarker and Individualized Therapy in Cancer	16F
	Moderator: Yau-Huei Wei, Ph.D. (魏耀揮校長)	
	Professor and President, Mackay Medical College, Taiwan	
16:10~16:40	Yu, Alice Lin-Tsing, M.D., Ph.D. (陳鈴津教授)	
	Cancer immunotherapy targeting tumor-associated glycans	
	Distinguished Chair Professor, Center of Stem Cells and Translational Cancer Research,	
16.40 17.10	Chang Gung Memorial Hospital and Chang Gung University, Taiwan	
10:40~17:10	Hongpin Ji, Fn.D. (孚紅砥研充貝)	
	YAP inhibits squamous transdifferentiation of Lkb1-deficient lung	
	adenocarcinoma through DNp63 repression	
	Chinese Academy of Sciences, China	
	Moderator: Jing-Jer Lin, Ph.D. (林敬哲教授)	
	Professor and Director, Graduate Institute of Biochemistry and Molecular Biology,	
	National Taiwan University, Taiwan	
17:10~17:40	Min-Liang Kuo, Ph.D. (郭明良教授)	
	A novel therapeutic target for treating hepatocellular carcinoma by	
	suppression vascular invasion and metastasis	
17 40 10 10	Professor and Director, College of Life Science, National Taiwan University, Taiwan	
17:40~18:10	Ronggui Hu, Ph.D. (胡榮貢研究員)	
	Iron metabolism regulates p53 signaling through direct heme-p53	
	Interaction and modulating localization, stability and function of p53	
	Chinese Academy of Sciences, China	
18:30~20:30	Banquet	
08:00~18:00	Exhibition 1F.	16F, B1
-)	







6/28 Day 2 (S	fat.)	
08:30~16:40	Registration	16F
	Session IV: Chromosome Instability in Cancer Development (II)	16F
	Moderator: <u>Mien-Chie Hung, Ph.D. (洪明奇院士)</u>	
	Academician, Academia Sinica, Taiwan Professor and Chain Department of Molecular and Collular Oroselecu	
	MD Anderson Cancer Center. The University of Texas. USA	
08.20~09.20	Astrid Gräslund, Ph.D.	
00.50 07.20	Ribonucleotide reductase- a dimetal/tyrosyl free radical enzyme	
	Academician, Royal Swedish Academy of Sciences	
00.00.00.00	Chairman, Dept. of Biochemistry and Biophysics, Stockholm University, Sweden K Kristoffor Andorsson Ph D	
09:20~09:50	Studies of the NrdF-NrdI complex and different metal ion clusters in	
	class I ribonucleotide reductases	
	Professor, Department of Biosciences, University of Oslo, Norway	
09:50~10:10	Coffee Break	16F/B1
	Moderator: <u>Jung-Yaw Lin, Ph.D. (林榮耀院士)</u>	
	Academician, Academia Sinica, Taiwan	
	Emeritus Professor, Department of Biochemistry, National Taiwan University, Taiwan	
10:10~10:40	Ming-Daw Isal, Ph.D. (祭明道院士)	
	Academician. Academia Sinica. Taiwan	
	Distinguished Research Fellow and Director, Institute of Biological Chemistry,	
10:10~10:40 10:40~11:10	Academia Sinica, Taiwan	
10:40~11:10	Hai Jiang, Ph.D. (姜海研究員)	
	Probing drug vulnerability associated with recurrent cancer genetic	
	lesions Professor Shanghai Institute of Biochemisrty and Cell Biology	
	Chinese Academy of Sciences, China	
11:10~11:40	Zee-Fen Chang, Ph.D. (張智芬教授)	
	Ribonucleotide reductase promotes the progression of genome	
	instability via dUTP-mediated replication stress	
	Professor and Director, Institute of Biochemistry and Molecular Biology, National Yang-Ming University Taiwan	
	Lunch	4 F
	Student Forum 14 位: 6 min/位	
	Moderator:	
	<u>Yau-Huei Wei, Ph.D. (魏耀揮校長)</u>	
11.50 12.25	Professor and President, Mackay Medical College, Taiwan	
11:50~15:25	Jung-Yaw Lin, Ph.D. (林榮耀院士)	
	Academician, Academia Sinica, Taiwan Emeritus Professor, Department of Biochemistry, National Taiwan University, Taiwan	
	Jacqueline Whang-Peng. M.D. (彭汪喜康院士)	
	Academician, Academia Sinica, Taiwan	
	Superintendent, Taipei Medical University Taipei Cancer Center, Taiwan	
	Session V: Stem Cell Research in Cancer	16F
	Moderator: Hua-Lin, Wu, Ph.D. (只要林教授)	
	National Cheng-Kung University. Taiwan	
13:25~13:55	Yun Zhao, Ph.D. (趙允研究員)	
	Decoding Ci: from partial degradation to inhibition	
	Professor, Shanghai Institute of Biochemisrty and Cell Biology,	
	Chinese Academy of Sciences, China	



13:55~14:25	B. Linju Yen, M.D. (顏伶汝副研究員)	
	Mechanisms involved in human mesenchymal stem cell (MSC)	
	immunomodulation: interactions with innate and adaptive leukocytes	
	Associate Investigator and Attending Physician, Institute of Cellular and Systems	
	Medicine, National Health Research Institutes, Taiwan Moderatory, Vy, Sun Chang, Dh. D. (25, 7, 4, 44, 48)	
	Mouerator: <u>Iu-Sun Chang, Fil.D. (派五生教校)</u> Professor Graduate Institute of Biomedical Sciences, Chang Cung University, Taiwan	
14:25~14:55	Ping Hu, Ph.D. (胡蘋研究員)	
	Activation of Wnt signaling prevents muscle atrophy	
	Professor, Shanghai Institute of Biochemisrty and Cell Biology, Chinase Academy of Sciences, China	
14:55~15:25	Ven-Hua Huang, Ph.D. (黃彥茲教授)	
11.55 15.25	Niche regulation of stemness expression in cancer	
	Professor and Director, Department of Biochemistry and Graduate Institute of Medical	
	Sciences, College of Medicine, Taipei Medical University, Taiwan	
15:25~15:45	Coffee Break	16F/B1
	Session VI: Translational Medicine in Cancer	16F
	Moderator: <u>Tao-Shih Hsieh, Ph.D. (謝道時院士)</u>	
	Academician, Academia Sinica, Taiwan	
	Biology, Academia Sinica, Taiwan	
15:45~16:15	Mien-Chie Hung, Ph.D. (洪明奇院士)	
	Novel signaling pathways in cancer cells and development of targeted	
	therapy	
	Academician, Academia Sinica, Taiwan	
	Professor and Chair, Department of Molecular and Cellular Oncology, MD Anderson	
16.15~16.45	Cancer Center, The University of Texas, USA Zhaocai Zhou Ph D (周兆士研究員)	
10.15 10.15	Development of a pentide-based VAP inhibitor sheds new light on	
	gastric cancer treatment	
	Professor, Shanghai Institute of Biochemisrty and Cell Biology,	
	Chinese Academy of Sciences, China	
	Moderator: <u>Jang-Yang Chang, M.D. (張俊彥院長)</u>	
	Professor and Dean, College of Medicine, National Cheng-Kung University, Taiwan	
	National Health Research Institutes. Taiwan	
16:45~17:15	Jing-Ping Liou, Ph.D. (劉景平教授)	
	Azaindolyl compounds with more selective inhibitory effect on histone	
	deacetylase 6 activity, exhibit antitumor activity in colorectal cancer	
	HCT116 cells	
	Professor and Associate Dean, School of Pharmacy, College of Pharmacy,	
17.15 17.15	Taipei Medical University, Taiwan	
17.15~17.45	Ann-Lii Cheng, M.D., Fli.D. (鄭女理教役) Mianaanganiam and aanaam A parisit of the spectrum of H	
	Nucroorganism and cancer: A revisit of the spectrum of <i>H</i> .	
	Professor and Director, Graduate Institute of Oncology. Collage of Medicine.	
	National Taiwan University, Taiwan	
17:45~18:15	Award & Closing Remark	16F
08:00~18:00	Exhibition 1F,	16F, B1







Map Information





Map Guidance



Roads & Streets

- A. 220 Lane, WuXing Street
- Β. Wusing Street(WuXing Street)
- 284 Lane, WuXing Street C.
- D. 22 Alley, 284 Lane, WuXing Street

Entrances

- i. University Entrance
- Hospital Entrance ii.
- Ambulance Entrance iii.

Buildings

- 1. Health Science Building
- Auditorium 2.
- 3. United Medical Building (Front Building)
- 4. United Medical Building (Back Building)
- 5. Oral Medicine Building
- Instruction Building 6.
- Medical Laboratory Science and Biotechnology Building A 7. Medical Laboratory Science and Biotechnology Building B
- 8.
- Morphology Building 9.
- 10. Gymnasium
- 11. Mushan Dormitory
- 12. First Building, Taipei Medical University Hospital
- 13. Second Building, Taipei Medical University Hospital
- 14. Third Building, Taipei Medical University Hospital







Transportation

TMU shuttle service

The school is located near MRT <u>Taipei City Hall (Blue Line)</u> and <u>Liuzhangli (Brown Line)</u> stations, and TMU provides shuttle services to both. Buses run every 15 minutes between the City Hall station and TMU (see route map), while the Liuzhangli shuttle bus runs every half an hour.



Public transit

Public transportation to TMU includes bus lines 266, 288, 226, 1, 235, 22, 33 and Blue 5.







Local Map









Floor Plan

報到動線 指示立牌 北醫工作人員 基金會工作人員 **VIP** 網 路 廠商攤位 報 名 學分 認證 現場 基金 報名 會 總務處 書寫區

United Medical Back Building, 1 FL.

United Medical Back Building, B1 FL.









United Medical Front Building, 4TH FL.



United Medical Back Building, 16F Lecture Hall











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Introduction of Moderator & Invited Speaker's Brief Curriculum Vitae and Abstract





Session I

Chromosome Instability in Cancer Development (I)

Moderator:

Yun Yen, M.D., Ph.D. (閻雲校長)



Distinguished Professor and President Taipei Medical University, Taiwan Dr. & Mrs. Allen Y. Chao Chair Developmental Cancer Therapeutics, City of Hope, U.S.A. Associate Director Translational Research, City of Hope, U.S.A. Chair and Professor Molecular Pharmacology, City of Hope, U.S.A. Professor Medical Oncology & Therapeutics Research, City of Hope, U.S.A. Co-leader Developmental Cancer Therapeutics, City of Hope, U.S.A.







Edward J. Benz, Jr. MD.

Academician, American Academy of Arts and Sciences National Academy of Sciences

President and CEO of Dana Farber Cancer Institute; Richard and Susan Smith Professor of Medicine, Genetics and Pediatrics, Harvard Medical School/Dana-Farber Cancer Institute

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Recent Selected Publications (Selected from >300 peer-reviewed publications): © Leto TL, Fortugno-Erikson, DM, Harris AS, Barton D, Yang-Feng TL, Francke U, Marchesi VT,

Benz EJ Jr. (1988) Comparison of non-erythroid α spectrin genes reveals strict homology among diverse species. *Mol Cell Biol* 8:1-9.

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Edward J. Benz Dana Farber Cancer Institute/ Harvard Medical School, USA

The combined effects of the sequencing of the human genome, the early success of targeted therapy with a signal transduction inhibitor (imatinib) for chronic myelogenous leukemia (CML), and the recognition that some targeted therapies were effective in diverse forms of cancer sharing similar molecular profiles have given rise to the hope that the treatment of individual cancer patients could be customized to attack the unique biological misbehaviors of his or her tumor. This approach has been variously termed "personalized cancer medicine", "individualized cancer medicine" or "high precision cancer medicine". The latter designation will be used in this presentation. In contrast to the first two terms, it does not pre-suppose that a unique therapy will be available for every patient, at least initially, nor does the term contaminate the broader interpersonal and psycho-social dimensions inherent in efforts to make care truly individualized and personalized. The earliest efforts to utilize molecular profiling of tumors to guide more precise therapies for individual patients have met with remarkable success in a few cases. Unfortunately, the paradigm has proven to be extraordinarily difficult to apply widely to most patients. There appear to be many reasons for this limited success. The tumors in many patients do not have obvious "driver" mutation against which a targeted agent is available; resistance against the (usually) single targeted agent can develop rapidly, etc. This presentation will review progress toward the achievement of high precision cancer treatments on a wide scale and on reflect one major cancer center's efforts to generate the necessary diagnostic information for precision therapy on an enterprise scale.







JoAnne Stubbe, Ph.D.



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Recent Selected Publications (Selected from >300 peer-reviewed publications):

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Radicals your life is in their hands: ribonucleotide reductases as a paradigm

JoAnne Stubbe Massachusetts Institute of Technology, USA

It will come as a surprise to many chemists and biologists, that Nature uses free radical chemistry in essential metabolic pathways. She has figured out how to harness the considerable reactivity of these species to carry out very difficult chemical transformations with exquisite specificity. I will discuss the role of "good" radicals in biology using ribonucleotide reductases (RNRs) as a paradigm, a problem that my lab has investigated for 30 years. Specifically we will give an overview of these complex enzymes: the complex, radical-mediated reduction chemistry, the radical initiation process that occurs over 35 angstroms, the biosynthetic pathways required for the essential dimetal-tyrosyl radical cofactor biosynthesis and maintenance, and the importance of deoxynucleotides and ATP in the regulation of quaternary structure which governs RNR activity. Each of these topics as a target for new anticancer therapeutics will be discussed.









Session I

Chromosome Instability in Cancer Development (I)

Moderator:



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Distinguished Professor Graduate Institute of Medical Sciences, Taipei Medical University, Taiwan

Director of the board Taipei Medical University, Taiwan





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Academician, Academia Sinica, Taiwan

Professor and President, China Medical University, Taiwan Donald Bren Professor of Biomedicine, Department of Biological Chemistry, University of California, Irvine, U.S.A. Email : whlee@mail.cmu.edu.tw

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Targeting tumor suppressor networks for therapeutic application

Wen-Hwa Lee China Medical University, Taiwan

An attractive approach to developing new anticancer drugs is to target genes or proteins that are essential for tumor cell growth and survival. Tumor suppressors play an essential role in the development of cancer. During the past decades, elucidation of fundamental function of tumor suppressors and its networks allows us to further explore its potentials for therapeutic application. The prototypic tumor suppressor, RB, a key cell cycle regulator, will serve as an example for this purpose. In addition, RB interacting protein, Hec1, which is a mitotic regulator, and a BRCA interacting protein, Rad51, which is a DNA recombinase, emerge as interesting targets. We have identified and generated derivatives of small compound inhibitors targeting these pathways and demonstrated the efficacy of these compounds. Furthermore, we have identified that IL17RB pathway plays an essential role in pancreatic cancer metastasis and generated neutralizing antibodies against IL17RB for blocking pancreatic cancer metastasis. This illustrates the differential approach based on the targets toward therapeutic application for cancer treatment.







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Ying Huang Shanghai Institute of Biochemisrty and Cell Biology, Chinese Academy of Sciences, China

Small-RNA-guided gene regulation is a common biological process in eukaryotic cells. Animal germ cells are characterized by an intriguing small-RNA-mediated gene-silencing mechanism known as PIWI pathway. PIWI-interacting RNAs (piRNAs) are small, 21-30 nt single-stranded RNAs that associate with PIWI proteins. The function of piRNA is silencing transposon elements in germ line cells to keep the genome integrity since germ line cells are the only source for transmitting genetic information to the next generation. For a long time the biogenesis of piRNA and the mechanism of how it functions remains unclear. The biogenesis of piRNAs is quite different from that of other small-RNA pathways, which is independent of Dicer. piRNA biogenesis occurs through both primary and secondary pathway (or called ping-pong cycle). In drosophila transcripts from heterochromatic clusters are processed into primary piRNAs. A particularly fast evolving homologue of heterochromatin protein 1 (HP1) called Rhino binds to dual-strand piRNA clusters and is required for their production. But how does Rhino recognize histone H3 trimethylated on lysine 9? What's the difference between Rhino and other HP1 proteins? Here we show the crystal structure of Rhino both in apo form and complex form with H3K9me3. We observed a unique dimer interface in Rhino and a domain-swapping in conformational change. These findings provide insights into the molecular mechanism of the specificity of Rhino recognizing histone H3K9me3 and its function in piRNA biogenesis.







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- Zong FY, Fu X, Wei WJ, Luo YG, Heiner M, Cao LJ, Fang Z, Fang R, Lu D, Ji H, Hui J. (2014) The RNA-binding protein QKI suppresses cancer-associated aberrant splicing. *PLOS Genet*, 10, e1004289
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Jingyi Hui Shanghai Institute of Biochemisrty and Cell Biology, Chinese Academy of Sciences, China

Lung cancer is the leading cause of cancer-related death worldwide. Aberrant splicing has been implicated in lung tumorigenesis. However, the functional links between splicing regulation and lung cancer are not well studied. To understand the role of RNA-binding proteins in lung tumorigenesis, we analyzed the public database and observed that RNA-binding protein QKI is down-regulated in non-small cell lung cancer (NSCLC) tissues and that its down-regulation is significantly associated with a poorer prognosis. Using a combined RNAi and RNA-Seq analysis, we identified several hundreds of alternatively spliced genes regulated by QKI and validated at least 24 lung cancer-related events in lung cancer tissues. We have obtained evidence that QKI inhibits cell proliferation through isoform-switch of its targets. To understand the mechanism of splicing regulation by QKI, we generated an RNA map of QKI and revealed that QKI can positively and negatively control exon inclusion in a binding-site position-dependent manner. We further showed that QKI inhibits splicing by selectively competing with a core splicing factor, SF1. Our findings demonstrate that QKI is a critical splicing regulator in lung cancer cells and contributes to lung tumorigenesis by modulating alternative splicing of its targets.











Session II

Cancer Metabolism and Signaling

Moderator:



Andrew H.-J. Wang, Ph.D. (王惠鈞院士)

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Computational modeling of IKK signaling

Anning Lin Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, China

IKK is essential for inhibition of TNF α -induced apoptosis. The survival role of IKK is thought to be mediated by activation of NF- κ B, which induces anti-apoptotic proteins (IAPs) and also prevents prolonged JNK1 activation. Recently, we found that phosphorylation and inactivation of pro-death Bcl-2 family protein BAD by IKK is required for cell survival upon TNF α stimulation, suggesting that activation of NF- κ B by IKK is necessary but not sufficient to suppress cell death. We will discuss the mathematic model that reveals the underlying mechanism by which IKK suppresses TNF α -induced apoptosis in the meeting.







Hsing-Jien Kung, Ph.D. (龔行健院士)

Academician, Academia Sinica, Taiwan

Professor, Institute for Translational Medicine, College of Medical Science and Technology, Taipei Medical University, Taiwan President and Distinguished Investigator, National Health Research Institutes Distinguished Professor (Emeritus), Dept. of Biochemistry & Molecular Medicine, University of California, Davis

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There is considerable evidence that tumor and normal cells differ in their metabolic requirements. The most prominent examples are the addiction of tumor cells to glucose (i.e., Warburg effect) and to glutamine. Therapeutics based on selective targeting of these metabolic pathways is under intensive investigations. Recently, we reported that irrespective of androgen receptor status, prostate cancer cells selectively and epigenetically suppress the expression of ASS (arginine succinosythethase), a rate-limiting enzyme for intracellular arginine synthesis. Analysis of over 100 PC specimens showed the complete absence of ASS expression, whereas some normal prostate epitheial cells express ASS. As a result, PC cells, but not normal counterparts become "auxotroph" for and addicted to external arginine. Thus, arginine-deprivation should selectively "starve" the PC cells to death. Indeed, in recent publications, we showed that depletion of external arginine by arginine deiminase (ADI) effectively induces cell death of CRPC cell lines, but not normal prostate epithelial cells in vitro and in vivo. In addition, we reported that ADI synergizes with Taxol in preclinical xenograft model. Based on this finding, a phaseI/II clinical trial is underway at UCD. Intriguingly, we found that ADI killing of cancer cells is associated with aggressive autophagy and appears to be caspase independent. At early phase, autophagy is protective and prolongs the survival of treated cells. Using high-resolution, live imaging, molecular and genetic profiling, we have now characterized in details the arginine-deprived cells undergoing apoptosis. The starved cells showed significant epigenetic reprogramming, excessive autophagy and most remarkably, nuclear rupture. The possible mechanism(s) and its implication will be discussed.











Session II

Cancer Metabolism and Signaling

Moderator:



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Molecular Pathways and Survival in Colorectal Cancer

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Colorectal cancers (CRC) display a large variety of somatic and germline genetic features that distinguish subsets of cancers with specific biologic behavior. Here we describe the results of a large, population-based study of 3,899 colorectal cancer cases and study these individuals to quantify CRC sub-types of clinical importance and to understand the relationships between molecular profiles and survival. Microsatellite instability, IHC expression of relevant MMR genes (MLH1, MSH2, MSH6, PMS2), founder and private germline mutations in the relevant genes and somatic mutations in the KRAS/BRAF or mTOR/PI3K signal transduction pathways all have potential prognostic and predictive implications and were assessed in tumor and germline DNA from all cases. Clinical and molecular annotation, combined with long term follow-up permitted multivariate survival analyses to identify the key molecular features associated with prognosis. Key findings will be presented.







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Genetic and hormonal contribution in breast cancer: tissue-specific tumor suppression by BRCA1

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Both the genetic make up and the endocrine system play crucial roles in breast carcinogenesis. Germ-line mutation in the tumor suppressor gene *BRCA1* increases the lifetime risk for breast cancer and ovarian cancer by up to ~80% and ~50%, respectively. Population-based studies support a sex- and tissue-specific tumor suppressor function of BRCA1, but the mechanisms of this specificity are not fully understood. Somatic loss of the normal functioning allele in BRCA1 carriers is common in cancer development and additional somatic events, including mutations of PTEN and TP53, occur at high frequencies. Studies of these carriers have found that breast cancer onsets in recent generations occur at much younger ages.

BRCA1 is ubiquitously expressed and has been found to play important roles in DNA replication and repair, cell cycle checkpoint control, in addition to its activity as a transcriptional regulator. We have identified a connection of BRCA1 mutations and stabilization of progesterone receptor (PR) through various pathways and an increased sensitivity of Brca1 deficiency to progesterone-induced mammary epithelial proliferation. Circadian oscillation influences many biological functions including sleep cycles, hormone secretion and cellular metabolism. A central circadian player, period 2 (Per2), is down regulated in Brca1/p53-deficienct mammary epithelial cells. Furthermore, Per-2 represses the expression of a group of genes critical for tumor progression. We also found how oxygen levels control the abundance of Per2 protein. In addition to decreased Per-2, some other contributing factors leading to earlier breast cancer onsets will be presented.











Session III

Biomarker and Individualized Therapy in Cancer

Moderator:



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Cancer immunotherapy targeting tumor-associated glycans

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Aberrant glycosylation is a feature of cancer cells. GD2, a disialoganglioside, is highly expressed in neuroblastoma, melanoma and small cell lung cancer and some sarcomas. Dr. Yu has pursued immunotherapy of neuroblastoma with a monoclonal anti-GD2 antibody, ch14.18, from preclinical studies to IND, phase I through phase III studies. The pivotal international phase III randomized trial in high risk neuroblastoma culminated in demonstrating that immunotherapy with ch14.18 + cytokines improved event free survival significantly from 46% \pm 5% to 66% \pm 5% (p=0.012) and overall survival from 75% \pm 5% to 86% \pm 4% at 2 yrs (p=0.022). This is the first time that a glycan is shown to be an effective target for cancer immunotherapy.

Another prevalent cancer associated glycan is Globo H, a hexasaccharide identified as a ceramide-linked glycolipid. It is overexpressed in a variety of common cancers including colon, ovarian, gastric, pancreatic, lung, prostate and breast cancers, but not detectable or only weakly expressed in limited normal tissues. Thus, it is an ideal target for cancer immunotherapy. Dr. Yu's group found Globo H to be present in breast cancer stem cells (BCSCs), although to a much lesser extent than non-BCSCs, in clinical breast cancer specimens. They also provided the first evidence for the expression of Gb5, the pentasaccharide precursor of Globo H, in BCSCs of >60% of tumors. Immunization of mice with Globo H-KLH and adjuvant induced antibody reactive with not only Globo H but also Gb5, suggesting that Globo H-based immunotherapy will target Globo H and Gb5-expressing tumor cells. Recently, they have uncovered a new aspect of immunosuppressive effects of Globo H ceramide (GHCer) which facilitate the escape of cancer cells from immune surveillance. The molecular processes involve down-regulation of Notch1 signaling at transcriptional level by ID3, and protein level through egr2/3 controlled *itch* expression. These data support the notion that GHCer plays dual roles in serving as a cancer-associated antigen, and as an immune checkpoint, further propelling the ongoing multi-national phase II/III clinical trial of globo H vaccine in breast cancer. In the meantime, a new generation of Globo H vaccine has been generated in collaboration with Dr. Wong's group by conjugating Globo H to diphtheria toxoid as a carrier protein and use of C34, a new analog of alpha-galactosylceramide (a-GalCer), as an adjuvant. The latter is a superior over α -GalCer, as reflected by its lack of α -GalCer- induced anergy and accumulation of myloid dervived suppressor cells. Further details will be discussed.







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Whether Hippo pathway contributes to cell lineage transition under pathological conditions, especially tumorigenesis, remains largely unknown. Through integrative studies on mouse models, human cancer cell lines and clinical specimens, we here find a distinct YAP activation pattern in lung adenocarcinoma(ADC) and squamous cell carcinoma(SCC); YAP is initially activated by LKB1 loss in lung ADC which represses DNp63 transcription in a default manner. During transdifferentiation, YAP is inactivated which in turn mediates default repression of DNp63 and triggers squamous differentiation reprogramming. Disruption of the YAP barrier for phenotypic transition significantly accelerates squamous transdifferentiation; constitutive activation of YAP conversely inhibits this transition. More importantly, ectopic DNp63 expression rescues the inhibitory effect of YAP upon squamous transdifferentiation. These findings have established YAP as an essential barrier for lung cancer cell fate conversion and provided a novel mechanism in phenotypic plasticity, which might hold important implication for YAP-targeted therapies.











Session III

Biomarker and Individualized Therapy in Cancer

Moderator:



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A novel therapeutic target for treating hepatocellular carcinoma by suppression vascular invasion and metastasis.

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Intra-hepatic vascular invasion of hepatocellular carcinoma (HCC) is the most important contributing factor to high recurrence and poor survival of patients. Here, we have identified leukocyte cell-derived chemotoxin 2 (LECT2) as a tumor suppressor that regulates hepatocellular carcinoma (HCC) vascular invasion and metastasis. LECT2 was inversely correlated with HCC recurrence and overall survival, and the expression of LECT2 was particularly high in non-vascular invasive samples. Furthermore, we employ a LECT2-affinity column plus LC-ms/ms to identify LECT2-binding proteins and found that MET receptor is strongly interacted with LECT2 protein. Despite the presence of HGF, the LECT2 binding causes an antagonistic effect to MET receptor activation through recruiting protein tyrosine phosphatase 1B (PTP1B). The antagonistic effect of LECT2 on MET activation also mainly contributes to the blockage of vascular invasion and metastasis of HCC. Our findings reveal a novel and specific inhibitory function of LECT2 in HCC via the direct binding and inactivation of MET, opening a potential avenue for treating MET-related cancer.







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Iron excess is closely associated with tumorigenesis in multiple types of human cancers, with underlying mechanisms yet unclear. Recently, iron deprivation has emerged as a major strategy for chemotherapy, but it exerts tumor-suppression only on select human malignancies. Here, we report that tumor suppressor p53 protein (p53) is downregulated during iron excess. Strikingly, heme, the iron polyporphyrin, binds to p53 protein, interferes with p53-DNA interactions and triggers nuclear export of p53 followed by cytosolic degradation. Moreover, in a tumorigenicity assay, iron deprivation suppressed tumor growth largely with dependence on wild-type p53, suggesting that upregulation of wild-type p53 signaling might critically underlie the selective efficacy of iron deprivation. Our findings thus identify the first direct link between iron/heme homeostasis and the regulation of p53 signaling, which not only provides mechanistic insights on tumorigenesis associated with iron excess, but may also help predict and improve outcomes in iron-deprivation based chemotherapy.










Session IV

Chromosome Instability in Cancer Development (II)

Moderator:



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Recent Selected Publications (Selected from >300 peer-reviewed publications):

- O Hammerstad M, Røhr AK, Andersen NH, Gräslund A, Högbom M, Andersson KK (2014) The class Ib ribonucleotide reductase from Mycobacterium tuberculosis has two active R2F subunits. J Biol Inorg Chem. Mar 2. [Epub ahead of print]
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Ribonucleotide reductase- a dimetal/tyrosyl free radical enzyme

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Transition metal ions like iron and manganese are important components of many enzymes. Diiron carboxylate enzymes are well-known participants in challenging redox reactions. Bacterial multicomponent monooxygenases and protein R2 of class I ribonucleotide reductase (RNR) are typical examples of such proteins.

In mammalian RNRs the enzymatic reaction is a bottleneck for providing the deoxyribonucleotide building blocks for DNA synthesis, both for DNA replication and repair. The mammalian class Ia RNR enzyme has two subunits, named proteins R1 and R2. The enzyme reduction reaction takes place in protein R1, but the activation of the enzyme depends on the diiron/tyrosyl free radical cluster in protein R2. The formation of the stable free radical on a tyrosine residue is a metal/oxygen dependent redox reaction. A long range proton coupled electron transfer (PCET) connects the radical site in R2 to the substrate binding site in R1.

Several inhibitors of the RNR enzyme, based on destruction of the stable tyrosyl free radical, have been identified. One such class of inhibitors is based on the activities of metal complexes of thiosemicarbazones (1).

Some years ago, a new class (Ic) of RNRs was identified in *Chlamydia trachomatis* (2). Electron Paramagnetic Resonance (EPR) spectroscopy studies showed that it lacks the tyrosyl radical found in other class I RNRs. As a metal cofactor this enzyme has a manganese/iron cluster instead of the common diiron cluster found in class Ia RNRs.

In class Ic RNR, the manganese/iron cluster has a similar function as the tyrosyl radical found in the R2 proteins of other class I RNRs. This function is to provide a shielded, reversible electron storage site during the enzymatic reaction, when the reduction of ribonucleotides takes place at the active site about 35Å away in protein R1.

The formation and catalytic activities of the manganese/iron cluster in this enzyme, as well as the EPR spectroscopic properties, have been characterized.

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Oxygen dependent ribonucleotide reductase (RNR) catalyzes the conversion of ribonucleotides to deoxyribonucleotides. The class Ia and Ib small subunit R2 carries a stable tyrosyl radical which is necessary for enzymatic activity[1]. We have studied the class Ib RNR R2F enzyme from Bacillus cereus, an opportunistic pathogen causing food poisoning, by light absorption, EPR, HF-EPR, CD, Raman, magnetic circular dicroism (MCD), and VTVH-MCD spectroscopy[2,3], in addition to 3D-structures obtained by protein crystallography of a R2F-NrdI complex[4]. We have also analyzed four different tyrosyl radicals from class Ia RNR from an anoxia tolerant carp[5] and one from Epstein-Barr virus[6]. In R2/R2F radicals, differences can be seen in rotational conformation of the phenoxyl rings and the presence of hydrogen bonds to phenyl-oxygens. We observed a tyrosyl-radical interacting with a di-manganese cluster in B. cereus R2F formed with the help of NrdI[7], similar to other class Ib R2Fs[8,9]. The manganese R2F has higher specific activity than the iron form with a thioredoxin reductant [10,11]. It seems we can obtain a tyrosyl radical interacting magnetically with other metal ions as well, such as Co(II). In the 3D-structure of iron-R2F-NrdI complex in B. cereus, we observe differences in the metal ion coordination site, as compared to the E. coli manganese-R2F-NrdI complex[4]. Interestingly, mammalian RNRs have both one R2 and one p53R2, carp RNR has two R2s and two p53R2s[5], while some bacteria can have two different R2Fs[12].

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Session IV

Chromosome Instability in Cancer Development (II)

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Recent Selected Publications (Selected from >300 peer-reviewed publications):

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Ming-Daw Tsai

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In this lecture I will present the use of structures to understand cancer signaling and DNA damage responses, on several subjects: the p16 family of tumor suppressor and their mutants identified in cancers; the histone demethylase RBP2; the tumor proliferation marker protein Ki67 and its binding with NIFK; the activation mechanism of human CHK2 and its yeast homolog Rad53 kinase. The role of FHA domain binding with phosphothreonine in the cancer related signaling and DNA damage responses will also be highlighted.





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Probing drug vulnerability associated with recurrent cancer genetic lesions

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Biomarkers that predict cancer cell's resistance or sensitivity to various drugs are essential for developing new anticancer drugs as well as designing personalized cancer treatment. Until now, most clinically relevant biomarkers are based on common oncogenes and tumor suppressors. Mutations of these genes have major impact on cancer cells, changing the gene expression profiles, signaling cascades and stress response, which can greatly influence their response to drugs. On the other hand, these genes are recurrently mutated in cancers to a certain rate, making it feasible to stratify cancer patients according to the status of these genes.

A common method of studying cancer mutation associated drug vulnerability is to subject a large panel of human cancer cell lines to genetic and drug sensitivity profiling. Through complicated bioinformatics analysis, drug sensitivities are assigned to certain genetic lesions. However, due to the complex nature of human cancer cell lines and high variability of drug sensitivity data, these approaches have recently been proven ineffective as means to study cancer mutation-associated drug vulnerability. Here we present a simpler yet reliable system to probe the genetic interactions between deregulated cancer genes and anticancer drugs. We will discuss how eipigenetic regulators recurrently mutated in human cancers might dictate drug response.







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The increase in RRM2A subunit of ribonucleotide reductase (RNR) expression is oncogenic and is closely associated with human cancers. It is unknown whether other nucleotide metabolic enzyme can counteract the oncogenic function of RNR. Overexpression of RRM2A is sufficient to induce replication stress, DNA damage signal and chromosome aberrations in mitosis, all of which are prevented by coexpression of dUTPase. Our mechanistic study showed that RRM2 overexpression increases the breaks in AT-rich fragile sites. Data from DNA fiber analysis revealed that elevation of RRM2A increases the rate of replication forks while impeding replication restart. Exogenous addition of thymidine or knockdown of uracil DNA glycosylase abolishes RRM2-induced aberration in replication restart, suggesting the implication of dUTP incorporation. In cancer cells, the context of high RRM2/low dUTPase exhibited higher level of DNA damage signal, and the clone evolved to metastasize with better growth fitness contains high RRM2/high dUTPase. Thus, high RRM2/low dUTPase might confer a cellular context promoting cancer evolution in preneoplasias and tumor tissues. In agreement, analysis of clinical samples also demonstrated that RRM2A interplays with dUTPase to affect colon and breast cancer survival.











Student Forum

Moderator:



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Session V

Stem Cell Research in Cancer

Moderator:



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Decoding Ci: from partial degradation to inhibition

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The evolutionarily conserved Hedgehog (Hh) signaling pathway is transduced by the Cubitus interruptus (Ci)/Gli family of transcription factors, which can be degraded either completely or partially from a full-length form (Ci155/GliFL) to a truncated repressor (Ci75/Gli^R) by proteasomes. The mechanism by which proteasomes distinguish ubiquitinated Ci/Gli to carry out complete versus partial degradation is not known. We show that Ter94/p97 ATPase is involved in processing Ci and Gli3 into Ci75 and Gli3^R. We demonstrate that Cul1-Slimb-based E3 ligase modifies Ci by efficient addition of K11-linked ubiquitin chains. Ter94^{Ufd1-like/dNpl4} complex interacts directly with Cull-Slimb, and, intriguingly, it prefers K11-linked ubiquitinated Ci. Thus, Ter94 ATPase and K11-linked ubiquitination in Ci contribute to the selectivity by proteasomes for partial degradation. In addition, aberrant activation of Hh signaling is associated with various human cancers, but the mechanism through which Ci^R/Gli^R properly represses target gene expression is poorly understood. We find that Atro directly binds to Ci through its C terminus. The N terminus of Atro interacts with a histone deacetylase, Rpd3, to recruit it to a Ci-binding site at the *decapentaplegic (dpp)* locus and reduce *dpp* transcription through histone acetylation regulation. The repressor function of Atro in Hh signaling is dependent on Ci. Furthermore, Rerea, a homologue of Atro in zebrafish, represses the expression of Hh-responsive genes. We propose that the Atro-Rpd3 complex plays a conserved role to function as a Ci^R corepressor.





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Mechanisms involved in human mesenchymal stem cell (MSC) immunomodulation: interactions with innate and adaptive leukocytes

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Despite the isolation of human embryonic stem cells (hESCs) and the more recently discovered induced pluripotent stem cells (iPS), many critical issues still surround these cells in terms of prevalent clinical use, the most important likely being the ethical concerns of hESC derivation, and tumorigenic potential of both these pluripotent stem cells. Increasing reports of plasticity for many adult stem cells (ASCs) have brought excitement and hope for broad therapeutic application, but these are rare cells and controversy still exists regarding ASC transdifferentiation capacity, especially to the extent of being clinically efficacious. Thus, the search continues for ethically conducive, easily accessible, and high-yielding source of stem cells. We have isolated and studied the immunobiology of novel sources of fetal-stage mesenchymal stem cells (MSCs), including placenta-derived multipotent cells (PDMCs) and hESC-derived mesenchymal progenitors. Fetal tissues are developmentally and immunologically more naïve than adult tissue, and often are discarded after the birth of the neonate, making this source ideal for isolation of progenitor cells for therapeutic use. We have found that these fetal-stage MSCs exhibit many markers common to adult bone marrow (BM) MSCs including CD105 and CD73, as well as hESC markers such as SSEA-4. Highly proliferative compared with adult BMMSCs, fetal-stage MSCs possess broader differentiation capacity than adult BMMSCs based on our recent data, and are strongly immunomodulatory towards allogeneic leukocytes. Mechanistically, suppression of allogeneic leukocytes by fetal-stage MSCs is largely due to secreted factors, and can be surprisingly enhanced with interferon- γ , a proinflammatory cytokine. The immunomodulation of fetal-stage MSCs extend to both innate and adaptive leukocytes, via mechanisms which we are interested in delineating for more efficacious clinical application of these versatile stem cells. With such broad immunosuppressive properties and multilineage differentiation capacity, fetal-stage MSCs may represent a potential cell source for therapeutic use.











Session V

Stem Cell Research in Cancer

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Activation of Wnt signaling prevents muscle atrophy

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Muscle is the most important organ for movements and metabolism. Maintenance of muscle mass in highly critical to keep muscle functions. Muscle atrophy is the most common pandemia in aged population. There is no efficacious medicine to prevent or treat muscle atrophy thus far. Therefore, the elucidation of the mechanism on muscle atrophy will shed light on developing medicines to prevent or treat muscle atrophy.

We found that Wnt signaling activities have changed dramatically upon muscle differentiation. Differentiated muscle fibers maintain significantly higher Wnt signaling levels compared to other organs. The increased Wnt signaling levels were achieved via decreased expression of of Wnt inhibitor Dickkopf3 (Dkk3). Inhibition of Wnt signaling in terminal differentiated muscle cells by DKK3 overexpression or small molecule inhibitors resulted in muscle atrophy. Further studies showed that Wnt signaling level could affect the binding profile of β -catenin on its target genes, thus resulting in selective activation of atrophy related genes.







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The expression of pluripotency-related genes in cells is linked to drug susceptibility which challenges the current therapy. Niche environment plays a critical role in stemness expression in cells either of embryonic or somatic stage. In somatic cancers, hepatocellular carcinoma (HCC) is an inflammation-associated cancer which is commonly associated with chronic hepatitis B virus (HBV) infection. We found the expression of pluripotency-related genes is regulated by IL-6-induced IGF/IGF-IR activation in HBV-HCC, and is associated with tumor aggressiveness and recurrence. In a large cohort of frozen HCC samples, we found significant correlation between IGF-IR and OCT4/NANOG transcriptional expressions and this association is preferentially found in hepatitis B virus (HBV)-related HCC (HBV-HCC) than those in non-HBV-HCC. Consistently, immunohistochemical staining showed significant positive correlation between the expressions of the OCT4/NANOG and the phosphorylation of IGF-IR in HCC tumor tissues. And, the stemness expression was significantly associated with tumor aggressiveness and poor disease-free survival (DFS). Niche IL-6 stimulated the expression of autocrine IGF-I and IGF-IR in a STAT-dependent manner, which stimulated the stemness-related properties in both the cell lines and the xenograft mouse tumors. The inhibition of the IGF-IR activation by RNA interference and molecular inhibitor significantly suppressed the IL-6-induced stemness-related properties in vitro and in vivo, suggesting that the IL-6-induced IGF-IR-mediated signaling is a potential target for individualized adjuvant therapy against HBV-HCC.

In embryonic stage, niche hypoxia down-regulated the OCT4 level and results in chemoresistance and poor prognosis in human pluripotent testicular germ cell tumors (TGCTs). Hypoxia reduces OCT4 levels and increases the resistance of embryonal carcinoma (EC) cells to cisplatin and bleomycin by regulating the SUMO1 peptidase SENP1. Overexpression of SENP1 reduced the Su-OCT4 level induced by SUMO1gg overexpression, thereby maintaining OCT4 levels and enhancing chemosensitivity. Mechanistic investigations revealed that OCT4 sumoylation occurred at K123, as overexpression of an OCT4-K123R mutant effectively reduced the level of Su-OCT4 under hypoxic conditions. These results demonstrated that hypoxia reduces OCT4 expression levels in pluripotent germ cell tumors to increase drug resistance, and these effects could be countered to ablate the suppressive effects of hypoxia on chemosensitivity.











Session VI

Translational Medicine in Cancer

Moderator:



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Novel signaling pathways in cancer cells and development of targeted therapy

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We discovered a non-canonical pathway of Hedgehog (Hh) through mTOR in addition to established, or canonical, pathway for activating Gli1 that both pathways converge to Gli1 leading to esophagus cancer. Crosstalk between these two pathways is a challenge, but our experiments showed a combination of the mTOR inhibitor RAD-001 (Everolimus®) and the Hedgehog inhibitor GDC-0449 (Erivedge®) steeply reduced the tumor burden in a mouse model of esophageal adenocarcinoma. GDC-0449, approved in January 2012 by the FDA for treatment of metastatic basal cell carcinoma, however, but in other cancers, such as ovarian and pancreas are resistant to GDC-0449. Our finding serve as a guidance for clinical trials of the combination for esophageal and other cancers including breast, ovarian and pancreatic cancers that could be directed by the antibody for phosphorylated Gli1 and the presence of plain Gli1, which would indicate a need to use both drugs (*Cancer Cell* 21, 374–387, 2012).

Previously, we have developed a targeted approach by developing a pancreatic cancer-specific expression vector (C-VISA) to treating pancreatic cancer with effective therapeutic efficacy and safety in noninvasive imaging models. Targeted expression of BikDD, a potent proapoptotic gene driven by C-VISA, exhibited significant antitumor effects on pancreatic cancer and prolonged survival in multiple xenograft and syngeneic orthotopic mouse models of pancreatic tumors with virtually no toxicity (*Cancer Cell* 12:52-65, 2007). A phase I IND protocol has been approved by the FDA in October 2010. A phase I clinical trial for advance pancreatic cancer patients will be initiated in 2012. Recently, we developed a breast cancer specific expression vector can specifically target breast cancer cells but not normal cells. Our study also presents a new strategy for killing breast cancer stem cells and for increasing their susceptibility to other therapies, thus lowering the chance of chemoresistance and recurrence (*Cancer Cell* 20:341-356, 2011). Cancer stem cells are a major culprit for drug resistance and recurrence. This study has important clinical implication and has been selected in the Leading Edge of Targeted Therapeutics in the Oct 14, 2011 issue of *Cell*.

In addition, we have recently identified an interesting mechanism showing how EGFR regulates DNA synthesis and repair through phosphorylation of histone H4. We have also identified a EGFR arginine methylation as a marker to predict resistance to cetuximab.







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Development of a peptide-based YAP inhibitor sheds new light on gastric cancer treatment

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The Hippo pathway has been implicated in suppressing tissue overgrowth and tumor formation by restricting the oncogenic activity of YAP. As an emerging significant player in tumorigenesis, the Hippo pathway has attracted increasing attention for the development of new anti-cancer drugs. In contrast to targeting upstream regulators such as MST1/2 and LATS, inhibition of YAP, the ultimate downstream effector of Hippo signaling, may provide a more effective and direct way to redress the Hippo pathway. However, transcriptional regulators that inhibit YAP activity have not been well studied. Here, we uncover clinical importance for VGLL4 in gastric cancer suppression and find that VGLL4 directly competes with YAP for binding TEADs. Importantly, VGLL4's tandem Tondu domains are not only essential but also sufficient for its inhibitory activity towards YAP. Our findings that VGLL4 is a natural antagonist of YAP and its TDU region is sufficient for YAP inhibition allowed for the development of a peptide-based YAP inhibitor. This peptide mimicking VGLL4 function potently suppresses gastric tumor growth in vitro and in vivo, providing an opportunity for treating gastric cancer which currently lacks effective treatment options. Collectively, our study indicates that disruption of YAP-TEADs interaction by a VGLL4-mimicking peptide may be a promising therapeutic strategy against YAP-driven human cancers.











Session VI

Translational Medicine in Cancer

Moderator:



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Azaindolyl compounds with more selective inhibitory effect on histone deacetylase 6 activity, exhibit antitumor activity in colorectal cancer HCT116 cells

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A series of indolylsulfonylcinnamic hydroxamates has been synthesized.**MPT0B291**, which has a 7-azaindole core cap, was shown to have antiproliferative activity against KB, H460, PC3, HSC-3, HONE-1, A549, MCF-7, TSGH, MKN45, HT29, and HCT116 human cancer cell lines. Pharmacological studies indicated that **MPT0B291** functions as a potent HDAC inhibitor with an IC_{50} value of 0.1 μ M. It is highly selective for histone deacetylase 6 (HDAC6) and is 60-fold more active than against HDAC1, 223-fold more active than against HDAC2. It has a good pharmacokinetic profile with oral bioavailability of 33%. In *in vivo* efficacy evaluations in colorectal HCT116 xenografts, **MPT0B291** suppresses tumor growth more effectively than SAHA and is therefore seen as a suitable candidate for further investigation









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Recent Selected Publications

- ◎ Tsai YC, Yeh CH, Tzen KY, Ho PY, Tuan TF, Pu YS, **Cheng AL**, Cheng JC (2013) Targeting epidermal growth factor receptor/human epidermal growth factor receptor 2 signalling pathway by a dual receptor tyrosine kinase inhibitor afatinib for radiosensitisation in murine bladder carcinoma. *Eur J Cancer* 49(6):1458-66.
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Microorganism and cancer: a revisit of the spectrum of *H. Pylori*-related gastric lymphoma

Ann-Lii Cheng National Taiwan University Taiwan

Low-grade mucosa-associated lymphoid tissue (MALT) lymphoma of the stomach (gastric MALT lymphoma) is associated with Helicobacter pylori infection. The eradication of H. pylori using antibiotics is successful in 60% to 80% of affected patients. In contrast to the previous paradigm, we and other investigators have shown that a certain proportion of patients with H. pylori-positive early-stage diffuse large B-cell lymphoma (DLBCL) of the stomach with histological evidence of MALT lymphoma (high-grade transformed gastric MALT lymphoma, gastric DLBCL[MALT]) achieved long-term complete pathological remission (pCR) after first-line H. pylori eradication therapy (HPE), indicating that the loss of H. pylori dependence and high-grade transformation are separate events in the progression of gastric lymphoma. In addition, patients with H. pylori-positive gastric DLBCL without histological evidence of MALT (gastric pure DLBCL) may also respond to HPE. A long-term follow-up study showed that patients who achieved pCR remained lymphoma-free. Gastric MALT lymphoma is indirectly influenced by H. pylori infection through T-cell stimulation, and recent studies have shown that H. pylori-triggering chemokines and their receptors, H. pylori-associated epigenetic changes, H. pylori-regulated microRNA expression, and tumor infiltration by CD4⁺CD25⁺ regulatory T cells contribute to lymphomagenesis of gastric MALT lymphoma. Recent studies have also demonstrated that the translocation of CagA into B lymphocytes inhibits apoptosis through p53 accumulation, BAD phosphorylation, and the upregulation of Bcl-2 and Bcl-X_L expression. In gastric MALT lymphoma, CagA may stimulate lymphomagenesis directly through the regulation of signal transduction, and intracellular CagA is associated with H. pylori dependence. These findings represent a substantial paradigm shift, compared with the classical theory of H. pylori-reactive T cells contributing indirectly to the development of MALT lymphoma. In conclusion, a wide range of H. pylori-related gastric lymphomas have been identified. The use of antibiotics as the sole first-line therapy for early-stage gastric pure DLBCL requires validation in a prospective study. The clinical and biological significance of the CagA oncoprotein in the lymphomagenesis of gastric MALT lymphoma warrants further study.







Poster Abstracts





103 年度第 11 屆海峽兩岸生物醫學獎摘要



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Education

2009.9-present	Ph.D. candidate, Shanghai Institute of Biochemistry and Cell
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2005.9-2009.7	B.S., Huazhong Agricultural University

Major Activities

Oral presentation: Regulation of miRNA processing by a multifunctional protein

YB-1. Cold Spring Harbor Asia Conferences-RNA Biology, Suzhou, 2012.

Honors and Awards

2013 Merit student, Chinese Academy of Sciences

Research Interests

miRNA biogenesis





Regulation of miRNA processing by a multifunctional protein YB-1

<u>Shuailai Wu (吳帥來)</u> and Jingyi Hui Shanghai Institute of Biochemistry and Cell Biology, CAS

MicroRNAs (miRNAs) are small non-coding RNAs that are key regulators of diverse cellular processes. Most miRNAs are generated from primary transcripts through two consecutive cleavage steps involving two RNase III enzymes: Drosha and Dicer. MiRNA maturation can be regulated at each individual step. However, the molecular mechanisms that regulate miRNA processing are largely unknown. The Y box-binding protein 1 (YB-1) is a member of the evolutionarily conserved nucleic acid binding protein family, which exhibits multiple functions in transcription, alternative splicing, mRNA stability, mRNA localization, and translation. YB-1 is overexpressed in many malignant tissues, and considered as a marker of tumorigenesis. Previously we characterized the CAUC sequence as an YB-1 binding motif with high affinity through a SELEX approach. Using iCLIP assay, we found that YB-1 also has a strong preference to bind CAUC motifs in vivo. We showed that specific binding of YB-1 to the terminal loop of miRNAs containing the CAUC motif influences the miRNA biogenesis. Overexpression of YB-1 in cultured cells inhibited the maturation of the miRNA. Using *in vitro* processing assays, we demonstrate that YB-1 interferes with the cleavages by Drosha and Dicer, respectively. Further analyses indicate that YB-1 blocks the accessibility of microprocessor and Dicer to the miRNA. Our study may provide a new mechanism for understanding the role of YB-1 in tumorigenesis.







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EDUCATION:
1999-2003: B.S in Veterinary Medicine, College of Veterinary Medicine, Inner Mongolia University for the Nationalities
2004-2007: M.S in Veterinary Medicine, College of Veterinary Medicine, Nanjing Agricultural University
2009-2013: Ph. D. in cellular biology, Shanghai Institute of Biochemistry and Cell Biology, CAS

HONOURS:

2012: The National Scholarship of China
2012: All around good Student of Chinese Academy of Science
2007: Outstanding thesis award of Jiangsu province of China
2002: Excellent Student Leaders of Inner Mongolia University for the Nationalities
2002: Professional third-class scholarship of Inner Mongolia University for the Nationalities
2001: Professional third-class scholarship of Inner Mongolia University for the Nationalities
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MAJOR RESEARCH INTERESTS:

My major research interests are lung cancer plasticity and it's functional correlation with drug resistance. With the integration of genomic studies of human lung cancer samples and functional biological studies using human cell lines and animal models, we plan to gain an insightful understanding of lung cancer biology and related mechanism, which potentially helps the development of better therapeutics in clinic. We have recently proven for the first time that mouse lung adenocarcinoma with Lkb1 deficiency could transit to squamous cell carcinoma via the mixed pathology as intermediate. We will continue to work on this project and translate our findings in animal models to human clinical samples.

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Lineage transition in adenocarcinoma (ADC) and squamous cell carcinoma (SCC) of non-small cell lung cancer (NSCLC), as implicated by clinical observation of mixed ADC and SCC pathologies in adenosquamous cell carcinoma (Ad-SCC), remains a fundamental yet unsolved question. Here we provide *in vivo* evidences showing the transdifferentiation of lung cancer from ADC to SCC in mice: *Lkb1*-deficient lung ADC progressively transdifferentiates into SCC, via pathologically mixed mAd-SCC as intermediate. We find that reduction of lysyl oxidase (Lox) in *Lkb1*-deficient lung ADC decreases collagen disposition and triggers extracellular matrix remodeling and eventually up-regulates *p63* expression, a SCC lineage survival oncogene. Pharmacological Lox inhibition promotes the transdifferentiation, whereas ectopic Lox expression significantly inhibits this process. Notably, ADC and SCC show differential responses to Lox inhibition. Collectively, our findings have discovered the *de novo* transdifferentiation of lung ADC to SCC in mice and provided mechanistic insight that may have important implications for lung cancer treatment.







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2010 年9月進入中國科學院上海生命科學研究所進行細胞生物學及發育生物學的研究,集神經與 Hedgehog 信號途徑在果蠅小腸幹細胞中的作用的研究。





Hh signaling in neurons controls intestinal stem cell fate in *Drosophila*

<u>Hui Han (韓暉)</u>, Chenyu Pan, Chunying Liu and Yun Zhao Shanghai Institute of Biochemistry and Cell Biology, CAS

Homeostasis of intestine is maintained by intestinal stem cells (ISCs) and their progenies, responding to various injuries. A complex autonomic nervous system spreads over intestine, however, whether and how neurons regulate intestine homeostasis is largely unknown. Here, we demonstrate that neurons contribute to the control of *Drosophila* intestinal homeostasis, and Hedgehog (Hh) signaling activity in neurons is essential for the determination of ISCs' fate. Downregulation of Hh signaling in neurons promotes ISCs' proliferation and inhibits their differentiation to enterocytes (ECs) while upregulation of Hh signaling in neurons promotes this differentiation process. Furthermore, Hh is secreted by enterocytes (ECs), offering a feedback signal to ISCs niche. Collectively, neuronal Hh signaling is essential for the determination of ISCs' fate.





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Educational History:

2008-2012 Shandong University School of Lifescience

2012-present Shanghai Institute of Biochemistry and Cell Biology

Research Interest:

Mechanisms and dynamics of TNF induced apoptosis





Mathematic modeling of IKK signaling network <u>Hao Zhang (張昊)</u>, Gaowei Wang, Xiang Yuan, Ping Ao and Anning Lin Shanghai Institute of Biochemistry and Cell Biology, CAS

The IkB kinase complex (IKK) is a key regulator of immune responses, inflammation, cell survival, and tumorigenesis. Recent studies revealed that IKK inhibits TNF α -induced apoptosis through two distinct but cooperative mechanisms: activation of NF- κ B signaling pathway and inactivation of the proapoptotic BH-3 only protein BAD. Here, we established a mathematic model to study the underling mechanism of IKK signaling. Using this model, we found that IKK signaling network obeys feedforward loop regulation mechanism. Both activation of NF- κ B and inactivation of BAD are necessary but not sufficient for IKK to suppress TNF α -induced apoptosis. Feedforward loop regulation mechanism also ensures the robustness and reversibility for IKK signaling network in prevention of TNF α -induced catastrophe.







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Education and Training

2004.9-2008.7	B.S.in Biological technology, Oceanography Institute, Shandong University
2008.9-now	M.S. & Ph.D. Shanghai Institute of Biochemistry and Cell Biology, CAS
Research Expe	rience
2011-now	Applications ProTA to identify mechanisms of drug action of Bortezomib and
	Carfilzomib, to identify mechanisms of HBV infection
2009-2011	Methodological and technical development for high-throughput ProTA (Protein
	<u>T</u> urnover <u>A</u> ssay)
2008-2009	Construction of the yeast genetic operation (The yeast two hybrid; gene
	knockout et al)

Invited Presentation

2013.05.18 The Eleventh National colloquium on the enzymatic, Wuxi. "ProTA(<u>Protein</u> <u>Turnover Assay</u>):Profiling human protein degradome to identify mechanisms of drug action and resistance"

Techniques

Recombinant DNA and genome engineering; Flow cytometry; Bioinformatics analysis for omic data; yeast and bacteria genetic operation (The yeast two hybrid;gene knockout; gene knockin et al); high-throughput experimentation; protein expression.

List of Publications

- Tao Yu, Yonghui Tao, Tao Zhang, Zi Chen, Meiqiang Yang, Peng Chen, Kangcheng Ruan, Yan Zhang, Ronggui Hu, Profiling human protein degradome delineates cellular responses to proteasomal inhibition and reveals a feedback mechanism in regulating proteasome homeostasis, Cell Research, 2014, in press.
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<u>Tao Yu (于濤)</u>, Yonghui Tao, Tao Zhang, Zi Chen, Meiqiang Yang, Peng Chen, Yan Zhang, Kangcheng Ruan and Ronggui Hu^{*}
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Global change in protein turnover (protein degradome) constitutes a central part of cellular responses to intrinsic or extrinsic stimuli. However, profiling protein degradome remains technically challenging. Recently, inhibition of proteasome, e.g. using Bortezomib (BTZ), has emerged as a major chemotherapeutic strategy for treating multiple myeloma and other human malignancies, but systematic understanding of the mechanisms for BTZ drug action and tumor resistance is yet to be achieved. Here we developed and applied a dual-fluorescence-based Protein Turnover Assay (ProTA) to quantitatively profile global changes in human protein degradome upon BTZ treatment. ProTA and subsequent network analyses delineates potential molecular basis for BTZ action and tumor drug resistance in BTZ chemotherapy. Finally, combined use of BTZ with drugs targeting the ProTA-identified key genes or pathways in BTZ action has overcome BTZ-resistance in multiple myeloma cells. Remarkably, BTZ stabilizes proteasome subunit (PSMC1) and proteasome assembly factor (PSMD10), suggesting a previously unappreciated mechanism for regulating proteasome homeostasis. Therefore, ProTA is emerging as a novel tool for profiling human protein degradome to elucidate potential mechanisms of drug action and resistance, which might facilitate therapeutic development targeting proteostasis to treat human disorders.





103 年度第 11 屆優秀論文獎摘要





Dual role for Islet-1 in promoting striatonigral and repressing striatopallidal genetic programs to specify striatonigral identity <u>Kuan-Ming Lu (盧冠名)</u>, Sylvia M. Evans, Shihji Hirano and Fu-Chin Liu Institute of Neuroscience, National Yang-Ming University

Striatal projection neurons comprise two populations of striatonigral and striatopallidal neurons. These two neuronal populations play distinct roles in controlling movement-related functions in the basal ganglia circuits. An important issue is how striatal progenitors are developmentally specified into these two distinct neuronal populations. In the present study, we characterized the function of Isl1, a LIM-homeodomain transcription factor, in striatal development. Genetic fate mapping showed that Isl1+ progeny specifically developed into a subpopulation of striatonigral neurons that transiently expressed Isl1. In Nestin-Cre;Isl1f/f knockout mouse brain, differentiation of striatonigral neurons was defective as evidenced by decreased expression of striatonigral-enriched genes. Striatonigral axonal projections were also impaired and abnormal apoptosis was observed in Isl1 knockout striatum. It was of particular interest that striatopallidal-enriched genes were concomitantly up-regulated in Isl1 mutant striatum, suggesting de-repression of striatopallidal genes in striatonigral neurons in the absence of Isl1. The suppression of striatopallidal genes by Isl1 was further examined by over-expression of Isl1 in the striatum of Drd2-EGFP transgenic mice using in utero electroporation. Ectopic Isl1 expression was sufficient to repress Drd2-EGFP signals in striatopallidal neurons. Our study suggests that Isl1 specifies the cell fate of striatonigral neurons not only by orchestrating survival, differentiation and axonal projections of striatonigral neurons, but also by suppressing striatopallidal-enriched genes. The dual action of developmental control by Isl1 in promoting appropriate striatonigral but repressing inappropriate striatopallidal genetic profiles may ensure sharpening the striatonigral identity during development.





Suberoylanilide hydroxamic acid (SAHA) causes tumor growth slowdown and triggers autophagy in glioblastoma stem cells <u>Ming-Tsang Chiao (</u>矯明昌), Wen-Yu Cheng, Yi-Chin Yang, Chiung-Chyi Shen and Jiunn-Liang Ko

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Although suberoylanilide hydroxamic acid (SAHA), a histone deacetylase inhibitor, has been used in clinical trials for cancer therapies, its pharmacological effects occur through a poorly understood mechanism. Here, we report that SAHA specifically triggers autophagy and reduces cell viability via promotion of apoptosis in the late phase of glioblastoma stem cells (GSC s). Using a cell line cultured from a glioblastoma biopsy, we investigated the properties and effects of GSC s under SAHA treatment in vitro. In vivo xenograft assays revealed that SAHA effectively caused tumor growth slowdown and the induction of autophagy. SAHA was sufficient to increase formation of intracellular acidic vesicle organelles, recruitment of LC3-II to the autophagosomes, potentiation of BEC N1 protein levels and reduced SQSTM1 levels. We determined that SAHA triggered autophagy through the downregulation of AKT-MTOR signaling, a major suppressive cascade of autophagy. Interestingly, upon depletion or pharmacological inhibition of autophagy, SAHA facilitates apoptosis and results in cell death at the early phase, suggesting that SAHA -induced autophagy functions probably act as a prosurvival mechanism. Furthermore, our results also indicated that the inhibition of SAHA -induced autophagy using chloroquine has synergistic effects that further increase apoptosis. Moreover, we found that a reduced dose of SAHA functioned as a potent modulator of differentiation and senescence. Taken together, our results provide a new perspective on the treatment of GSC s, indicating that SAHA is a promising agent for targeting GSC s through the induction of autophagy.







Hexamethonium reverses the lethal cardiopulmonary damages in

a rat model of brainstem lesions mimicking

fatal Enterovirus 71 encephalitis

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OBJECTIVES: Among enterovirus 71 infections, brainstem encephalitis progressing abruptly to cardiac dysfunction and pulmonary edema causes rapid death within several hours. However, no currently known early indicators and treatments can monitor or prevent the unexpectedly fulminant course. We investigate the possible mechanisms and treatment of fatal enterovirus 71 infections to prevent the abrupt progression to cardiac dysfunction and pulmonary edema by using an animal model.

DESIGN: Treatment study. SETTING: Research laboratory. SUBJECTS: Sprague-Dawley rats.

INTERVENTIONS: We microinjected 6-hydroxydopamine or vitamin C into nucleus tractus solitarii of the rat and evaluated the cardiopulmonary changes after treatment with ganglionic blocker.

MEASUREMENTS AND MAIN RESULTS: The time course of changes in the heart and lungs of rats with brainstem lesions were investigated. Rats were administered 6-hydroxydopamine to induce brainstem lesions, causing acute hypertension in 10 minutes and acute elevations of catecholamines accompanied by acute cardiac dysfunction and increased strong expressions of connexin 43 gap junction protein in heart and lung specimens by immunohistochemical staining within 3 hours. Severe pulmonary hemorrhagic edema was produced within 6 hours, and the rats expired rapidly within 7 hours. After hexamethonium treatment, it was found that the acute hypertension induced by 6-hydroxydopamine lesions was immediately reversed and the acute high rise of catecholamine serum level was significantly attenuated within 3 hours, accompanied by preserved cardiac output and decreased expressions of connexin 43 in the heart and lungs. No pulmonary edema occurred and the rats survived for more than 14 hours.

CONCLUSIONS: Early hexamethonium treatment attenuates acute excessive release of catecholamines to prevent cardiac dysfunction and pulmonary edema for increasing survival rate.





Recombinant protein rVP1 upregulates BECN1-independent autophagy, MAPK1/3 phosphorylation and MMP9 activity via WIPI1/WIPI2 to promote macrophage migration <u>Chiao-Chun Liao (廖皎君)</u>, Ming-Yi Ho, Shu-Mei Liang and chi-Ming Liang Graduate Institute of Life Sciences, National Defense Medical Center Institute of Biological Chemistry, Academia Sinica

The monocyte/macrophage is critical for regulating immune and antitumor responses. Recombinant capsid protein VP1 (rVP1) of foot-and-mouth disease virus induces apoptosis and inhibits migration/metastasis of cancer cells. Here, we explored the effects of rVP1 on macrophages. Our results showed that rVP1 increased LC3-related autophagosome formation via WIP11 and WIP12 in a BECN1-independent manner. rVP1 treatment increased macrophage migration that was attenuated by knockdown of ATG5, ATG7, WIP11 or WIP12 and was abolished when both WIP11 and WIP12 were depleted. Treatment of macrophages with rVP1 increased matrix metalloproteinase-9 (MMP9) activity and phosphorylated mitogen-activated protein kinase 1/3 (MAPK1/3), two major mediators of cell migration. Knockdown of WIP11, WIP12, ATG5 and ATG7 but not BECN1 attenuated the rVP1-mediated increase in MAPK1/3 phosphorylation and MMP9 activity. These results indicated that rVP1 upregulated autophagy, MAPK1/3 phosphorylation and MMP9 activity to promote macrophage migration, which was dependent on WIP11, WIP12, ATG5 and ATG7 but not BECN1.





CTGF increases drug resistance to paclitaxel by upregulating survivin expression in human osteosarcoma cells <u>Hsiao-Chi Tsai (蔡筱琪)</u>, Chun-Yin Huang, Hong-Lin Su and Chih-Hsin Tang National Chung Hsing University China Medical University

Osteosarcoma is the most common primary malignant tumor, and its treatments require more effective therapeutic approaches. Paclitaxel has a broad range of antitumor activities, including apoptosis-inducing effects. However, the majority of tumors in patients with advanced cancer eventually develop chemoresistance. Connective tissue growth factor (CTGF) is a secreted protein that modulates the invasiveness of certain human cancer cells by binding to integrins. However, the effect of CTGF in paclitaxel-mediated chemotherapy is unknown. Here, we report that the expression of CTGF in osteosarcoma patients was significantly higher than CTGF expression in normal bone tissues. Overexpression of CTGF increased the resistance to paclitaxel-mediated cell apoptosis. In contrast, knockdown of CTGF expression by CTGF shRNA increased the chemotherapeutic effect of paclitaxel. In addition, CTGF increased resistance to paclitaxel-induced apoptosis through upregulation of survivin expression. Moreover, the AMP-activated protein kinase (AMPK)-dependent nuclear factor kappa B (NF-KB) pathway mediated paclitaxel-increased chemoresistance and survivin expression. In a mouse xenograft model, overexpression of CTGF promoted resistance to paclitaxel. In contrast, knockdown of CTGF expression increased the therapeutic effect of paclitaxel in this model. In conclusion, our data indicate that CTGF might be a critical oncogene of human osteosarcoma involved in resistance to paclitaxel treatment.





Cytotoxicity, oxidative stress, apoptosis and the autophagic effects of silver nanoparticles in mouse embryonic fibroblasts <u>Yu-Hsuan Lee (李宥菅)</u>, Fong-Yu Cheng, Hui-Wen Chiu, Jui-Chen Tsai,

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With the advancement of nanotechnology, nanomaterials have been comprehensively applied in our modern society. However, the hazardous impacts of nanoscale particles on organisms have not yet been thoroughly clarified. Currently, there exist numerous approaches to perform toxicity tests, but common and reasonable bio-indicators for toxicity evaluations are lacking. In this study, we investigated the effects of silver nanoparticles (AgNPs) on NIH 3T3 cells to explore the potential application of these nanoparticles in consumer products. Our results demonstrated that AgNPs were taken up by NIH 3T3 cells and localized within the intracellular endosomal compartments. Exposure to AgNPs is a potential source of oxidative stress, which leads to the induction of reactive oxygen species (ROS), the upregulation of Heme oxygenase 1 (HO-1) expression, apoptosis and autophagy. Interestingly, AgNPs induced morphological and biochemical markers of autophagy in NIH 3T3 cells and induced autophagosome formation, as evidenced by transmission electron microscopic analysis, the formation of microtubule-associated protein-1 light chain-3 (LC3) puncta and the expression of LC3-II protein. Thus, autophagy activation may be a key player in the cellular response against nano-toxicity.





Optogenetic control of selective neural activity in multiple freely moving Drosophila adults

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We present an automated laser tracking and optogenetic manipulation system (ALTOMS) for studying social memory in fruit flies (Drosophila melanogaster). ALTOMS comprises an intelligent central control module for high-speed fly behavior analysis and feedback laser scanning (~40 frames per second) for targeting two lasers (a 473-nm blue laser and a 593.5-nm yellow laser) independently on any specified body parts of two freely moving Drosophila adults. By using ALTOMS to monitor and compute the locations, orientations, wing postures, and relative distance between two flies in real time and using high-intensity laser irradiation as an aversive stimulus, this laser tracking system can be used for an operant conditioning assay in which a courting male quickly learns and forms a long-lasting memory to stay away from a freely moving virgin female. With the equipped lasers, channelrhodopsin-2 and/or halorhodopsin expressed in selected neurons can be triggered on the basis of interactive behaviors between two flies. Given its capacity for optogenetic manipulation to transiently and independently activate/inactivate selective neurons, ALTOMS offers opportunities to systematically map brain circuits that orchestrate specific Drosophila behaviors.





Enhancement of ADP release from the RAD51 presynaptic filament by the SWI5-SFR1 complex

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Homologous recombination catalyzed by the RAD51 recombinase eliminates deleterious DNA lesions from the genome. In the presence of ATP, RAD51 forms a nucleoprotein filament on single-stranded DNA, termed the presynaptic filament, to initiate homologous recombination-mediated DNA doublestrand break repair. The SWI5-SFR1 complex stabilizes the presynaptic filament and enhances its ability to mediate the homologous DNA pairing reaction. Here we characterize the RAD51 presynaptic filament stabilization function of the SWI5-SFR1 complex using optical tweezers. Biochemical experiments reveal that SWI5-SFR1 enhances ATP hydrolysis by single-stranded DNA-bound RAD51. Importantly, we show that SWI5-SFR1 acts by facilitating the release of ADP from the presynaptic filament. Our results thus provide mechanistic understanding of the function of SWI5-SFR1 in RAD51-mediated DNA recombination.





Histone demethylase retinoblastoma binding protein-2 promotes lung tumorigenesis and cancer metastasis

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The retinoblastoma binding protein-2 (RBP2), a demethylase capable of removing the dior tri-methyl group from lysine 4 of histone 3, promotes gastric cancer cell growth and is enriched in drug-tolerant lung cancer cells. The gene knockout study further suggests that RBP2 loss suppresses tumor initiation in mice lacking the tumor suppressor Rb or MEN1. Nevertheless, the direct link of RBP2 to tumorigenesis and the underlying mechanism are unclear. Here we attack the question by exploring the role of RBP2 in lung cancer. We show that RBP2 was overexpressed in human lung cancer tissues and that RBP2 depletion impaired lung cancer cell proliferation, motility, migration, invasion and metastasis. Mechanistically, the oncogenic potential of RBP2 depended on its demethylase and DNA contact activities. Moreover, RBP2 upregulated the expressions of cyclins D1 and E1, while suppressed the expression of cyclin-dependent kinase inhibitor p27, likely contributing to RBP2-mediated lung cancer cell proliferation. Microarray analysis further revealed that RBP2 promoted the expression of integrin beta 1 (ITGB1), a membrane receptor involved in cancer metastasis through cell adhesion and recognition. RBP2 directly bound to p27, cyclin D1, and ITGB1 promoters and the exogenous cyclin D1, cyclin E1 or ITGB1 expression rescued cell proliferation and migration/invasion, respectively, reduced by RBP2 knockdown. Taken together, these results not only demonstrate a positive role of RBP2 in lung tumorigenesis and metastasis, but also uncover novel RBP2 targets for the oncogenic function of RBP2. Targeting RBP2 may provide a useful therapeutic strategy in lung cancer treatment.







Chromosome 19 open reading frame 80 is upregulated by the thyroid hormone and modulates autophagy and lipid metabolism

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The thyroid hormone, T₃, regulates cell growth, differentiation and development through binding to the nuclear thyroid hormone receptor (THR), a member of the steroid/THR superfamily of ligand-dependent transcriptional factors. T₃ modulates lipid metabolism in liver, although the detailed molecular mechanisms are unclear at present. Here, by a microarray analysis we identified a novel *chromosome 19 open reading frame 80 (C19orf80)* which was activated by T₃. T₃ stimulation led to upregulation of both mRNA and protein levels of *C19orf80*. Immunofluorescence analysis revealed a vesicle-like pattern of C19orf80 around lipid droplets or within the lysosome-associated compartment in cells. Furthermore, T₃ treatment as well as C19orf80 overexpression specifically activated the autophagic response and lipid metabolism, as observed from lipidated LC3 (LC3-II) and levels of oxygen consumption rate, respectively. Reciprocally, knockdown of C19orf80 obstructed T₃-activated autophagy and lipolysis. Moreover, treatment with autolysosome maturation inhibitors, ammonium chloride and chloroquine, not only suppressed the T₃-activated autophagic process but also lipid metabolism. Our results collectively suggest that T₃ regulates lipid metabolism through a C19orf80-activated autophagic process.





Instructive nanofiber scaffolds with VEGF create a microenvironment for arteriogenesis and cardiac repair <u>Hsin-Chieh Wu (吳欣潔)</u>, Yu-Ching Lin, Cheng-Hsin Liu, Hsiang-Ching Chung, Ya-Ting Wang, Ya-Wen Lin, Hsin-I. Ma, Pang-Hsien Tu, Sean E. Lawler and Ruey-Hwa Chen Graduate Institute of Life Sciences, National Defense Medical Center Institute of Biological Chemistry, Academia Sinica

The promyelocytic leukaemia (PML) protein controls multiple tumour suppressive functions and is downregulated in diverse types of human cancers through incompletely characterized post-translational mechanisms. Here we identify USP11 as a PML regulator by RNAi screening. USP11 deubiquitinates and stabilizes PML, thereby counteracting the functions of PML ubiquitin ligases RNF4 and the KLHL20-Cul3 (Cullin 3)-Roc1 complex. We find that USP11 is transcriptionally repressed through a Notch/Hey1-dependent mechanism, leading to PML destabilization. In human glioma, Hey1 upregulation correlates USP11 and PML downregulation and with high-grade malignancy. with The Notch/Hey1-induced downregulation of USP11 and PML not only confers multiple malignant characteristics of aggressive glioma, including proliferation, invasiveness and tumour growth in an orthotopic mouse model, but also potentiates self-renewal, tumour-forming capacity and therapeutic resistance of patient-derived glioma-initiating cells. Our study uncovers a PML degradation mechanism through Notch/Hey1-induced repression of the PML deubiquitinase USP11 and suggests an important role for this pathway in brain tumour pathogenesis.





Spontaneous seroclearance of Hepatitis B seromarkers and subsequent risk of hepatocellular carcinoma

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Background and Aims: The associations between long-term risk of hepatocellular carcinoma (HCC) and spontaneous seroclearance of hepatitis B virus (HBV) e antigen (HBeAg), HBV DNA, and HBV surface antigen (HBsAg) have never been examined by a prospective study using serially measured seromarkers. This study aimed to assess the importance of spontaneous HBeAg, HBV DNA, and HBsAg seroclearance in the prediction of HCC risk.

Methods: This study included 2,946 HBsAg seropositive individuals who were seronegative for antibodies against hepatitis C virus and free of liver cirrhosis. Serial serum samples collected at study entry and follow-up health examinations were tested for HBeAg, HBV DNA and HBsAg. Cox proportional hazards models were used to calculate the hazard ratios of developing HCC after seroclearance of HBV markers.

Results: The hazard ratio (95% confidence interval) of developing HCC after seroclearance of HBeAg, HBV DNA and HBsAg during follow-up was 0.63 (0.38-1.05), 0.24 (0.11-0.57), and 0.18 (0.09-0.38), respectively, after adjustment for age, gender and serum level of alanine aminotransferase at study entry. High HBV DNA levels at the seroclearance of HBeAg (mean \pm standard deviation, $4.35 \pm 1.64 \log 10 \text{ IU/mL}$) may explain the non-significant association between HBeAg seroclearance and HCC risk. Among HBeAg-seronegative participants with detectable serum HBV DNA at study entry, the lifetime (30-75 years old) cumulative incidence of HCC was 4.0%, 6.6% and 14.2%, respectively, for those with seroclearance of both HBV DNA and HBsAg, seroclearance of HBV DNA only, and seroclearance of neither.

Conclusions: Spontaneous seroclearance of HBV DNA and HBsAg are important predictors of reduced HCC risk.







The role of LMBRD1 in regulating cardiac insulin signaling Linda Tzu-Ling Tseng (曾子玲), Chieh-Liang Lin, Kai-Yuan Tzen, Shin C Chang and Ming-Fu Chang Institute of Biochemistry and Molecular Biology, National Taiwan University

Energy homeostasis is crucial in maintaining normal biological functions of cells. Disturbances in such balance often lead to various diseases. Limb region 1 (LMBR1) domain containing 1 gene (*lmbrd1*) encodes a nine-transmembrane LMBD1 protein. Previous study demonstrated that double allele frameshift mutation of *lmbrd1* is associated with lysosomal cobalamin export deficiency, suggesting the participation of LMBD1 in the export of cobalamin from lysosome to the cyotsol. In this study, we have distinguished that heterozygous deletion of *lmbrd1* is sufficient for causing cardiac diseases through a pathway independent of the vitamin B12 metabolic defect. Imbrd1 ubiquitous heterozygous knockout *Imbrd1*^{+/-} mice exhibited increase in myocardial glucose uptake and insulin receptor signaling that were insensitive to the administration of additional insulin. Consistent with the constitutively activated insulin receptor signaling, *lmbrd1*^{+/-} mice exhibited an increase in heart rate and cardiac muscle contractility, leading to the development of compensated pathological hypertrophy and fibrosis. As *lmbrd1*^{+/-} mice aged, the decrease in ejection fraction and fraction shortening showed signs of ventricular function deterioration. Additional studies using primary ventricular cells demonstrated that knockdown of *lmbrd1* resulted in an elevated signaling of insulin receptor (IR) and its downstream molecule Akt. Confocal and live total internal reflection fluorescence microscopy showed that LMBD1 colocalized and co-internalized with clathrin and IR upon insulin induction. Mutagenesis and phenotypic rescue studies further identified the motifs responsible for assisting the endocytosis of IR. Altogether, LMBD1 plays a regulatory role in the plasma membrane as an adaptor protein for insulin receptor endocytosis and modulates the IR metabolic signaling pathway.





SUMOylated CPAP is required for IKK-mediated NF-κβ activation and enhances HBx-induced NF-κβ signaling in HCC.

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Background & Aims: Constitutive activation of NF- κ B is an important event involved in chronic inflammation in hepatocellular carcinoma (HCC). CPAP, which plays important roles in centrosomal functions, was previously identified as the transcriptional co-activator of NF- κ B. However, the molecular mechanism is unclear. The goal of this study was to investigate the role of CPAP in activating the NF- κ B pathway in HCC.

Methods: SK-Hep1, HuH7, HepG2, HepG2X, Hep3B, and Hep3BX cells with CPAP overexpression or *CPAP* siRNA were used to evaluate activation of NF- κ B under TNF- α stimulation by reporter assay, RT-PCR, Q-PCR, and Western blot analysis. *In vivo* SUMO modification of CPAP was demonstrated by an *in situ* PLA assay. Human HCC tissues were used to perform Q-PCR, Western blot, and IHC.

Results: *CPAP* siRNA abolished the interaction between IKK β and NF- κ B, whereas overexpression of CPAP enhanced this interaction and finally led to augmented NF- κ B activation by increasing the phosphorylation of NF- κ B. CPAP could enter nuclei by associating with NF- κ B. Furthermore, CPAP was SUMO-1 modified upon TNF- α stimulus, and this is essential for its NF- κ B co-activator activity. SUMO-1-deficient CPAP mutant lost its NF- κ B coactivator activity and failed to enter nuclei. Importantly, SUMOylated CPAP could synergistically increase the HBx-induced NF- κ B activity.

Conclusions: CPAP is essential for the recruitment of the IKK complex to inactivated NF- κ B upon TNF- α treatment. Expression of CPAP was positively correlated with a poor prognosis in HBV-HCC. CPAP has the potential to serve as a therapeutic target for inflammation and inflammation-related diseases.





The contribution of mitochondrial thymidylate synthesis in preventing the nuclear genome stress <u>Ming-Hsiang Lee (李明祥)</u>, Liya Wang and Zee-Fen Chang Institute of Biochemistry and Molecular Biology, College of Medicine, National Taiwan University

In quiescent fibroblasts, the expression levels of cytosolic enzymes for thymidine triphosphate (dTTP) synthesis are down-regulated, causing a marked reduction in the dTTP pool. In this study, we provide evidence that mitochondrial thymidylate synthesis via thymidine kinase 2 (TK2) is a limiting factor for the repair of ultraviolet (UV) damage in the nuclear compartment in quiescent fibroblasts. We found that TK2 deficiency causes secondary DNA double-strand breaks formation in the nuclear genome of quiescent cells at the late stage of recovery from UV damage. Despite slower repair of quiescent fibroblast deficient in TK2, DNA damage signals eventually disappeared, and these cells were capable of re-entering the S phase after serum stimulation. However, these cells displayed severe genome stress as revealed by the dramatic increase in 53BP1 nuclear body in the G1 phase of the successive cell cycle. Here, we conclude that mitochondrial thymidylate synthesis via TK2 plays a role in facilitating the quality repair of UV damage for the maintenance of genome integrity in the cells that are temporarily arrested in the quiescent state.





The tyrosine kinase Syk differentially regulates Toll-like receptor signaling downstream of the adaptor molecules TRAF6 and TRAF3

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Toll-like receptors (TLRs) are a major family of pattern-recognition receptors and they play a crucial role in innate immunity. Several reports have suggested that spleen tyrosine kinase (Syk) mediates signaling by TLRs; however, the mechanisms involved are unclear. We found that Syk was not only involved in the endocytosis of TLR4, but that it also played a dual role in TLR4-mediated signaling. Stimulation of TLR4 by its ligand lipopolysaccharide (LPS) led to the enhanced activation in Syk-deficient macrophages of the kinase TAK1, which is required for proinflammatory cytokine production, compared to that in wild-type macrophages. In contrast, Syk-deficient macrophages exhibited decreased TLR4-dependent activation of the TBK1-IRF3 pathway, which is required for the production of type I interferons. These two arms of TLR4 signaling, the proinflammatory TAK1-dependent pathway and the immunmodulatory TBK1-dependent pathway, are downstream of complexes containing the E3 ubiquitin ligases TRAF6 and TRAF3, respectively. We found that Syk was present in both TRAF6- and TRAF3-containing signaling complexes; however, the LPS-dependent, lysine-63-linked ubiquitination of TRAF6 and TRAF3 was oppositely regulated by Syk. We also identified the domains of Syk that interacted with TRAF3, TRAF6, TAK1, and TBK1, thus suggesting the role of Syk as a common regulator of various TLR responses. Together, our results demonstrate the opposing regulatory roles of Syk in TLR4-mediated TRAF6 and TRAF3 signaling pathways, which leads us to suggest that Syk may fine-tune the innate immune response to lessen inflammation.

Furthermore, we demonstrate that although Syk negatively controls LPS-induced pro-IL-1 β expression, it is a positive regulator of NLRP3 inflammasome activation. Taken together, our results demonstrate the opposite regulatory roles of Syk in TLR4-mediated TRAF6 and TRAF3 signaling pathways, as well as in IL-1 β production through pro-IL-1 β gene expression and NLRP3 inflammasome activation.





A negative feedback of the HIF-1α pathway via interferon-stimulated gene 15 and ISGylation <u>Yen-Hsiu Yeh (葉彥秀)</u>, Yu-Chen Yang, Mei-Yi Hsieh, Yen-Cheng Yeh and Tsai-Kun Li Department and Graduate Institute of Microbiology, College of Medicine, National Taiwan University

Because cancer has become the highest mortality among diseases, researchers around the world are committed to uncover the potential tumorigenic mechanisms and related intervention of concurring cancer. In recent years, inflammation has regarded as the enhancing characteristics of cancer hallmarks and been proven to contribute to tumor initiation and progression. Inflammation, like hypoxia microenvironment, is also a critical factor for a variety of diseases such as heart disease, stroke and diabetes. Here, we have investigated interactions between microenvironments and relation with cancer development. We found that ISG15 (interferon-stimulated gene 15) modulates hypoxia-inducible factor-1 α (HIF-1 α) functions. ISG15 conjugation (ISGylation) and ubiquitylation systems play critical roles in hypoxic inflammation. Interferon and hypoxia-mimetic desferoxamine were used to induce ISG15 and HIF-1 α expression respectively and to study effects of ISG15 on the HIF-1 α activity. We observed free-form HIF-1 α is regulated by interferon, and expression of ISG15 is lower in the hypoxic state. Further mechanistic investigation reveals HIF-1 α not only physically interacts with ISG15 but also is a substrate for ISGylation at multiple sites. Overexpression of ISG15 disrupted HIF- 1α /HIF1 β dimerization and subsequently HIF-1a-induced gene expression and tumor growth in xenograft mouse models were attenuated by ISG15 and ISGylation expression. Based on the above results, we concluded and proposed a novel negative feedback mechanism of hypoxia where ISG15 regulates HIF-1 α via ISGylation.




Repression of miR-126 and up-regulation of ADM in the stromal endothelium confers angiogenesis of cervical cancer. <u>Tien-Hung Huang (黄田宏)</u> and Tang-Yuan Chu Center for Cervical Cancer Prevention, Department of Research, Tzu Chi General Hospital Institute of Medical Science, Tzu Chi University

miR-126 is an endothelial-specific microRNA essential for maintaining vessel integrity during development. Its role of tumor angiogenesis in cancer stroma is unclear. This study investigated the temporal and spatial expression and the role of miR-126 in the course of cervical carcinogenesis. miR-126 was found to be mainly expressed in the stromal endothelium of the uterine cervix. This downregulation was recapitulated in a cell coculture model, wherein cross talk of cervical cancer cells and fibroblasts induced a downregulation of miR-126 in human umbilical vein endothelial cells, with consequent increase of tube formation. Coinjection of cancer-associated fibroblasts of human cervix enhanced tumorigenesis of cervical cancer cells, with an increase of microvessel density and dye retention in the tumor vasculature. In association with angiogenesis, host-originated miR-126 in these xenograft tumors was progressively downregulated, whereas supplement of the miR-126 precursor in the coinjection suppressed angiogenesis and tumor growth. A proangiogenic gene adrenomedullin (ADM), which was found to be upregulated in the stroma of cervical cancer and which localized mainly in the blood and lymphatic vessels, was identified as a target of inhibition by miR-126 at the carcinoma in situ-to-invasion stage. The study suggests a cancer stroma cross talk induced repression of miR-126 and upregulation of ADM, and probably other proangiogenic factors, to facilitate angiogenesis and invasion growth of cervical cancer.





Teroxirone inhibited growth of human non-small cell lung cancer cells by activating p53

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In this work, we demonstrated that the growth of human non-small-cell-lung-cancer cells H460 and A549 cells can be inhibited by low concentrations of an epoxide derivative, teroxirone, in both in vitro and in vivo models. The cytotoxicity was mediated by apoptotic cell death through DNA damage. The onset of ultimate apoptosis is dependent on the status of p53. Teroxirone caused transient elevation of p53 that activates downstream p21 and procaspase-3 cleavage. The presence of caspase-3 inhibitor reverted apoptotic phenotype. Furthermore, we showed the cytotoxicity of teroxirone in H1299 cells with stable ectopic expression of p53, but not those of mutant p53. A siRNA-mediated knockdown of p53 expression attenuated drug sensitivity. The in vivo experiments demonstrated that teroxirone suppressed growth of xenograft tumors in nude mice. Being a potential therapeutic agent by restraining cell growth through apoptotic death at low concentrations, teroxirone provides a feasible perspective in reversing tumorigenic phenotype of human lung cancer cells.





Hypomethylation signature of tumor-initiating cells predicts poor prognosis of ovarian cancer patients

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DNA methylation contributes to tumor formation, development, and metastasis. Epigenetic dysregulation of stem cells is thought to predispose to malignant development. The clinical significance of DNA methylation in ovarian tumor-initiating cells (OTICs) remains unexplored. We analyzed the methylomic profiles of OTICs (CP70sps) and their derived progeny using a human methylation array. qRT-PCR, quantitative methylation-specific PCR (qMSP), and pyrosequencing were used to verify gene expression and DNA methylation in cancer cell lines. The methylation status of genes was validated quantitatively in cancer tissues with clinicopathological factors. ATG4A and HIST1H2BN were and correlated hypomethylated in OTICs. Methylation analysis of ATG4A and HIST1H2BN by qMSP in 168 tissue samples from patients with ovarian cancer showed that HIST1H2BN methylation was a significant independent predictor of progression-free survival (PFS) and overall survival (OS). Multivariate Cox regression analysis showed that patients with a low level of HIST1H2BN methylation had poor PFS (HR, 4.5; 95% CI, 1.4–14.8) and OS (HR, 4.3; 95% CI, 1.3–14.0). Hypomethylation of both ATG4A and HIST1H2BN predicted a poor PFS (HR, 1.8; 95% CI, 1.0-3.6; median, 21 months) and OS (HR, 1.7; 95% CI, 1.0-3.0; median, 40 months). In an independent cohort of ovarian tumors, hypomethylation predicted early disease recurrence (HR, 1.7; 95% CI, 1.1–2.5) and death (HR, 1.4; 95% CI, 1.0–1.9). The demonstration that expression of ATG4A in cells increased their stem properties provided an indication of its biological function. Hypomethylation of ATG4A and HIST1H2BN in OTICs predicts a poor prognosis for ovarian cancer patients.







Epigenetic silencing of PTPRR activates MAPK signaling, promotes metastasis and serves as a biomarker of invasive cervical cancer

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Epigenetic modifications are a driving force in carcinogenesis. However, their role in cancer metastasis remains poorly understood. The present study investigated the role of DNA methylation in cervical cancer metastasis. Here, we report evidence of the overexpression of DNA methyltransferases 3B (DNMT3B) in invasive cervical cancer and of the inhibition of metastasis by DNMT3B interference. Using methyl-DNA immunoprecipitation coupled with microarray analysis (mDIP-on-chip), we found that the protein tyrosine phosphatase receptor type R (PTPRR) was silenced through DNMT3B-mediated methylation in cervical cancer. PTPRR inhibited p44/42 MAPK signaling, the expression of the transcription factor AP1, human papillomavirus (HPV) oncogenes E6/E7, and DNMTs. The methylation status of PTPRR increased in cervical scrapings (n = 358) in accordance with disease severity, especially in invasive cancer. Methylation of the PTPRR promoter plays an important role in the metastasis and may be a biomarker of invasive cervical cancer.

已通過之專利:

- 名稱:一種癌症的篩檢方法 Cancer Screening Method:
- (國家/Application No./Filing Date)
- 1.台灣 / 098112589 / Apr 16 2009
- 2.中國大陸 / 200910135501.X / Apr 17 2009
- 3. PCT / PCT/CN2009/000411 / Apr 17 2009
- 4.美國 / 12/543,400 / Aug 18 2009





Prostate cancer-derived CCN3 induces M2 macrophage infiltration and contributes to angiogenesis in prostate cancer microenvironment <u>Po-Chun Chen (陳栢均)</u>, Hsu-Chen Cheng, John Wang, Shin-Wei Wang,

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Tumor-associated macrophages (TAMs) are M2-polarized macrophages that infiltrate the tumor microenvironment and promote tumorigenesis. However, the mechanisms by which TAMs modulate prostate cancer (PCa) growth are poorly understood. Here, we found that expression of Nephroblastoma Overexpressed (NOV/CCN3) is upregulated in PCa cells and correlated with M2 macrophage infiltration. RAW264.7 macrophage migration was induced by conditioned media (CM) from various PCa cells in proportion to the cellular level of CCN3 expression and was inhibited by an anti-CCN3 neutralizing antibody. CCN3 and PCaCM treatment skewed RAW264.7 cell differentiation from an M1 phenotype to an M2 phenotype. PCa-derived CCN3 induced focal adhesion kinase (FAK)/Akt/NF-κB signaling in RAW264.7 cells, which resulted in VEGF expression and subsequently increased tube formation in endothelial progenitor cells. Finally, PCa-secreted CCN3 stimulated RAW264.7 cells and promoted angiogenesis in the chick chorioallantoic membrane assay (CAM), and increased tumor growth and tumor-associated angiogenesis in a PCa xenograft mouse model. Our results indicate that PCa-secreted CCN3 can recruit macrophages and skew their differentiation to an M2 phenotype. In turn, CCN3-stimulated macrophages contribute to VEGF-dependent angiogenesis. This study reveals a novel mechanism by which TAMs enhance PCa angiogenesis and identifies a potential therapeutic target for PCa.







Suppression of the SOX2 neural effector gene by PRDM1 promotes human germ cell fate in embryonic stem cells <u>I-Ying Lin (林依登)</u>, Feng-Lan Chiu, Chen-Hsiang Yeang, Hsin-Fu Chen, Ching-Yu Chuang, Shii-Yi Yang, Pei-Shan Hou, Nardnisa Sintupisut, Hong-Nerng Ho, Hung-Chih Kuo and Kuo-I Lin National Yang-Ming University Genomics Research Center, Academia Sinica

The mechanisms of transcriptional regulation underlying human primordial germ cell (PGC) differentiation are largely unknown. The transcriptional repressor Prdm1/Blimp-1 is known to play a critical role in controlling germ cell specification in mice. Here, we show that PRDM1 is expressed in developing human gonads and contributes to the determination of germline versus neural fate in early development. We show that knockdown of PRDM1 in human embryonic stem cells (hESCs) impairs germline potential and upregulates neural genes. Conversely, ectopic expression of PRDM1 in hESCs promotes the generation of cells that exhibit phenotypic and transcriptomic features of early PGCs. Furthermore, PRDM1 suppresses transcription of *SOX2*. Overexpression of *SOX2* in hESCs under conditions favoring germline differentiation skews cell fate from the germline to the neural lineage. Collectively, our results demonstrate that PRDM1 serves as a molecular switch to modulate the divergence of neural or germline fates through repression of *SOX2* during human development.





優秀論文獎編號: PhD24

Regulation of mitochondrial F₀F₁ATPase activity by Sirt3-catalyzed deacetylation and its deficiency in human cells harboring 4977bp deletion of mitochondrial DNA <u>Yu-Ting Wu (吳雨亭)</u>, Hsin-Chen Lee, Chen-Chung Liao and Yau-Huei Wei Department of Biochemistry and Molecular Biology,

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Sirt3, a mitochondrial NAD(+)-dependent deacetylase, is regarded as a potential regulator in cellular metabolism. However, the role of Sirt3 in the regulation of mitochondrial F_0F_1ATP as and the linkage to mitochondrial diseases is unclear. In this study, we demonstrated a role of Sirt3 in the regulation of F_oF₁ATPase activity in human cells. Knockdown of Sirt3 in 143B cells by shRNA transfection caused increased acetylation levels of the α and OSCP subunits of F₀F₁ATPase. We showed that Sirt3 physically interacted with the OSCP and led to its subsequent deacetylation. By incubation of mitochondria with the purified Sirt3 protein, Sirt3 could regulate F₀F₁ATPase activity through its deacetylase activity. Moreover, suppression of Sirt3 reduced the F_0F_1ATP as activity, consequently decreased the intracellular ATP level, diminished the capacity of mitochondrial respiration, and compromised metabolic adaptability of 143B cells to the use of galactose as the energy source. In human cells harboring ≅85% of mtDNA with 4977bp deletion, we showed that oxidative stress induced a reduction of Sirt3 expression, and an increased acetylation of the OSCP subunit of F₀F₁ATPase. Importantly, the expression of Sirt3 was also decreased in the skin fibroblasts from patients with CPEO syndrome. We further demonstrated that oxidative stress induced by 5-10µM of menadione impaired the Sirt3-mediated deacetylation and activation on F₀F₁ATPase activity through decreasing the protein level of Sirt3. Our findings suggest that increased intracellular ROS levels might modulate the expression of Sirt3 which deacetylates and activates F₀F₁ATPase in human cells with mitochondrial dysfunction caused by a pathogenic mtDNA mutation.





Chemotherapeutic sensitivity of testicular germ cell tumors under hypoxic conditions is negatively regulated by SENP1-controlled sumoylation of OCT4.

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Testicular germ cell tumors (TGCT) generally respond well to chemotherapy, but tumors that express low levels of the transcription factor OCT4 are associated with chemoresistance and poor prognosis. Hypoxia is known to induce drug resistance in TGCTs; however, the mechanistic basis for reduced expression of OCT4 and drug resistance is unclear. Here we show that hypoxia reduces OCT4 levels and increases the resistance of embryonal carcinoma (EC) cells to cisplatin and bleomycin. Furthermore, we show that the loss of OCT4 expression under hypoxia can be triggered by sumoylation, which was regulated by SUMO1 and the SUMO1 peptidase SENP1. Under hypoxic conditions, overexpression of SUMO1gg (the active form of SUMO1) not only increased the level of sumoylated OCT4 (Su-OCT4), but also decreased the stability of OCT4 protein. In addition, overexpression of SENP1 reduced the Su-OCT4 level induced by SUMO1gg overexpression, thereby maintaining OCT4 levels and enhancing chemosensitivity. Mechanistic investigations revealed that OCT4 sumoylation occurred at K123, as overexpression of an OCT4-K123R mutant effectively reduced the level of Su-OCT4 under hypoxic conditions. Taken together, our results showed that hypoxia reduces OCT4 expression levels in ECs to increase drug resistance and that these effects could be countered to ablate the suppressive effects of hypoxia on chemosensitivity. Our findings also highlight SENP1 as a potential therapeutic target for drug resistant TGCTs.





優秀論文獎編號: PhD26

Innovative strategy with potential to increase hemodialysis efficiency and safety

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Uremic toxins are mainly represented by blood urine nitrogen (BUN) and creatinine (Crea) whose removal is critically important in hemodialysis (HD) for kidney disease. Patients undergoing HD have a complex illness, resulting from: inadequate removal of organic waste, dialysis-induced oxidative stress and membrane-induced inflammation. Here we report innovative breakthroughs for efficient and safe HD by using a plasmon-induced dialysate comprising Au nanoparticles (NPs)-treated (AuNT) water that is distinguishable from conventional deionized (DI) water. The diffusion coefficient of $K_3Fe(CN)_6$ in saline solution can be significantly increased from 2.76 to 4.62×10^{-6} cm s⁻¹, by using AuNT water prepared under illumination by green light-emitting diodes (LED). *In vitro* HD experiments suggest that the treatment times for the removals of 70% BUN and Crea are reduced by 47 and 59%, respectively, using AuNT water instead of DI water in dialysate, while additionally suppressing NO release from lipopolysaccharide (LPS)-induced inflammatory cells.





Putative oncogene *UBE1C* inhibits the transcription activity of p53 in lung cancer

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Background: In view of the therapeutic benefits resulting from early intervention for Fabry disease, our team has implemented an enzyme-based newborn screening in Taiwan since 2008. However, we found that most heterozygous females cannot be detected. To improve the screening efficiency, a more effective method for *GLA* gene genotyping is necessary.

Methods: As the suspected mutations are limited to only 29 different spots in Taiwanese, a panel of Sequenom iPLEX assay was designed for rapid screening of *GLA* variations. To determine the accuracy and sensitivity of this assay, previously diagnosed and undiagnosed DNA samples were analyzed by this genotyping assay and Sanger sequencing. In addition, DNA extracted from dried blood spots was also tested.

Results: Sequenom iPLEX assay is accurate and cost-effective, identifying the sequence variations, which were designated in the panel. It identified common *GLA* variants in DNA samples extracted from whole blood or dried blood spots with 100% accuracy and sensitivity.

Conclusions: Sequenom iPLEX assay is suitable for Fabry newborn screening when hotspot mutations and common variations are known in a well-studied population. In addition, this assay can also be applied for first-line determination of *GLA* variant sequences in suspected subjects of high-risk patients, or newborns.

Keywords: Fabry disease; Sequenom's MassARRAY[®]; Sequenom iPLEX assay; *GLA* genotyping.





優秀論文獎編號: MS6

Quantitative apical membrane proteomics reveals vasopressin-induced actin dynamics in collecting duct cells <u>Chin-San Loo (呂振山)</u>, Cheng-Wei Chen , Po-Jen Wang, Pei-Yu Chen, Shu-Yu Lin, Kay-Hooi Khoo, Robert A. Fenton, Mark A. Knepper and Ming-Jiun Yu Institute of Biochemistry and Molecular Biology,

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In kidney collecting duct cells, filamentous actin (F-actin) depolymerization is a critical step in vasopressin-induced trafficking of aquaporin-2 to the apical plasma membrane. However, the molecular components of this response are largely unknown. Using stable isotope-based quantitative protein mass spectrometry and surface biotinylation, we identified 100 proteins that showed significant abundance changes in the apical plasma membrane of mouse cortical collecting duct cells in response to vasopressin. Fourteen of these proteins are involved in actin cytoskeleton regulation, including actin itself, 10 actin-associated proteins, and 3 regulatory proteins. Identified were two integral membrane proteins (Clmn, Nckap1) and one actin-binding protein (Mpp5) that link F-actin to the plasma membrane, five F-actin end-binding proteins (Arpc2, Arpc4, Gsn, Scin, and Capzb) involved in F-actin reorganization, and two actin adaptor proteins (Dbn1, Lasp1) that regulate actin cytoskeleton organization. There were also protease (Capn1), protein kinase (Cdc42bpb), and Rho guanine nucleotide exchange factor 2 (Arhgef2) that mediate signal-induced F-actin changes. Based on these findings, we devised a live-cell imaging method to observe vasopressin induced F-actin dynamics in polarized mouse cortical collecting duct cells. In response to vasopressin, F-actin gradually disappeared near the center of the apical plasma membrane while consolidating laterally near the tight junction. This F-actin peripheralization was blocked by calcium ion chelation. Vasopressin-induced apical aquaporin-2 trafficking and forskolin-induced water permeability increase were blocked by F-actin disruption. In conclusion, we identified a vasopressin-regulated actin network potentially responsible for vasopressin-induced apical F-actin dynamics that could explain regulation of apical aquaporin-2 trafficking and water permeability increase.









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Transcriptional activation of pentraxin-3 gene expression is associated with EGF-induced head and neck cancer cell metastasis Shuo-Lun Wu (吳碩倫), Jhih-Peng Tsai and Ben-Kuen Chen Institute of Bioinformatics and Biosignal Transduction, College of Bioscience and Biotechnology, National Cheng-Kung University

Overexpression of epidermal growth factor receptor (EGFR) and production of proinflammatroy cytokines are well clarified in head and neck squamous cell carcinoma (HNSCC) and correlates with enhanced invasion and metastasis. However, molecular mechanisms involved in activation of EGFR and productions of cytokines in regulating metastasis of HNSCC remain poorly understood. Here, we identified PTX3 as a metastasis-promoting factor to mediate EGF-induced HNSCC metastasis. Analysis of PTX3 expression between normal and malignant or metastatic tissues from HNSCC patients was performed using published datasets, indicating that expression level of PTX3 in malignant tissues was higher than in normal part in HNSCC patients. We found that EGF induced transcriptional activation of PTX3 by activating the binding of c-Jun and NF-kB factors to AP-1 binding site of the PTX3 promoter. The downstream of EGFR pathways, PI3K/AKT and NF-kB were essential for the induction of PTX3. In addition, EGF- induced PTX3 expression was significantly inhibited in c-Jun and NF-KB knockdown cells. EGF stimulated the secretion of PTX3 from cancer cell, resulting in enhancing cell migration and invasion. Effects of EGF on the induction of fibronectin and MMP9 expression, and inhibition of E-cadherin were abolished in PTX3 knockdown cells. These findings reveal the mechanism that autocrine production of EGF-induce PTX3-regulated HNSCC metastasis was through enhancing metastatic molecules, such as fibronectin and MMP9 expression. Induction of PTX3 possibly reflecting the EGFR-caused HNSCC metastasis associated with inflammation.





Annexin A2 regulates epithelial-mesenchymal transition and therapeutic tolerance in nasopharyngeal carcinoma <u>Chang-Yu Chen (陳昌佑)</u>, Yin-Ju Chen, Yun-Tien Lin, Fang-Yi Cheng, Shao-Te Yeh, Yun-Ho Lin, Pin-Zhir Chao and Chien-Ho Chen School of Medical Laboratory Science and Biotechnology, Taipei Medical University

Nasopharyngeal carcinoma (NPC), originated from the epithelium of the nasopharynx, is a common malignant tumor. NPC mainly occurs in the Southeast Asia including Taiwan. Characteristically, NPC is different from other head and neck carcinomas, especially for its high metastasis character and poor efficiency of clinical treatment. Recently, many reports have indicated that annexin A2 might regulate the metastasis on different kinds of cancer. However, the tumorigenic function of annexin A2 in NPC is not yet understood. According to our data, the level of annexin A2 highly expressed on NPC patient tissues by using immunohistochemistry (IHC). Annexin A2 shRNAs were used to evaluate the effects of annexin A2 suppression on NPCs. Silencing annexin A2 protein reduces the cell proliferation both in vivo and in vitro. Moreover, annexin A2 regulates the tolerance to chemo drugs (Cisplatin, 5-FU, Vincristine and Docetaxel) and irradiation. From chemo drug killing assay and radio survival assay, annexin A2 knockdown cell line (781) shows more sensitive to chemo- and radio reaction compared to scramble control. Furthermore, Annexin A2 not only up-regulates cell adhesion, migration, and invasion abilities on NPCs, but also involves in epithelial-mesenchymal transition (EMT). In summary, annexin A2 regulates the EMT pathway and therapeutic tolerance in NPCs. We believe that annexin A2, on nasopharyngeal carcinoma, may be a prognosis target during clinical therapy.





Role of EPAEE in improving response and specific target drug sensitivity in KRAS mutated cells <u>Li-Wei Kuo (郭力瑋)</u>, Wen-Hui Weng, Bi-Qiang Huan and Wai-Hung Leung Graduate Institute of Biochemical and Biomedical Engineering,

National Taipei University of Technology

EPA ethyl ester (EPAEE) is known easily absorbed and obtained from fatty fish. In current study, we provide a possible therapeutic strategy to the colorectal cancer (CRC), which was known when the cells contain with the KRAS mutant is a activating predominate mechanism of resistance to EGFR inhibitors, Erbitux. According to our pervious findings, up-regulated the expression of miR-A by intaking lauric acid in mutant CRC cells would further triggered the cells sensitive to Erbitux. Herein, we used FDA-approved EPAEE instead of lauric acid, and try to give a practical purpose of clinical application. We hypothezied that increase the concentration of EPAEE might result in the cell proliferation, which might modulate expression of miR-A, and further effect the protein phosphorylation of ERK1/2, and then further trigger the effect of Erbitux to mutants CRC cells. Obviously, higher expression of miR-A could be detected after treated with 40µM EPAEE for 24 hours in all type of mutated cells except control wild type CRC cells. In addition, the lower cell survival rate has been observed in the 0.2µM of Erbitux treatment, especially in the KRAS mutants and control wild type cells (p= 0.010~0.013). Interestingly, the higher phosphorylated proteins level of ERK1/2 could be noted in KRAS EPAEE-fed cells (p=0.006~0.047), although the total protein was shown lower expression level (p=0.035); but opposite result was shown in BRAF EPAEE-fed mutants when compared to original cells. Consist of higher Erbitux response rate in KRAS mutants and even in Caco-2 could also be found. However, less evidences in BRAF mutant CRC cells could be observed might result from few case collections. Indeed, unclear bio-mechanism of EPAEE need to be further proved. In conclusion, up-regulation of the miR-A induced by EPAEE might further lead KRAS mutant cells significantly restored the sensitivity to Erbitux. Our findings might offer great potential of therapeutic solution for future clinical CRC patients.





To study the role of CCN1 in neointima formation <u>Jheng-Sin Chen (陳正鑫)</u> Department of Cell Biology and Anatomy, College of Medicine, National Cheng Kung University

CCN1 (Cyr61), an extracellular matrix protein, is involved in diverse and sometimes opposing cellular activities through binding to a variety of integrins in different cell types and contexts. Vascular remodeling occurs preferentially at branched or curved arteries with disturbed flow leading to low and oscillatory wall shear stress. Despite the close association between CCN1 and neointima formation, the role of CCN1 in neointima formation-induced by disturbed flow is not clear. In this study, we used the mouse models induced by complete carotid artery ligation to identify the role of CCN1 in neointima formation. First, Ccn1+/LacZ mice, in which a LacZ gene was inserted in the Ccn1 genomic locus to be driven by Ccn1 promoter, were used to identify the CCN1 expression in neointima formation after carotid artery ligation. After ligation, CCN1 was expressed in neointima and media of the ligated artery. We will use the markers of endothelial cell, smooth muscle cell and macrophage to identify the types of cells expressing CCN1. Second, we speculate CCN1 may affect the neointima formation via binding to integrin $\alpha 6\beta 1$, so we used $Ccn 1^{dm/dm}$ mice (DM), which express $\alpha 6\beta$ 1-binding deficient CCN1 protein. After ligation, we found that the neointima area in DM mice was less developed than in WT mice. This result indicated that $\alpha 6\beta$ 1-binding deficient mutation of Ccn1 attenuates neointima formation following blood flow cessation. Next. understand how CCN1 reduces neointima formation. will to we use immunofluorescence staining to indicate whether CCN1 mediates the expression of adhesion molecules, immune cells infiltration, the secretion of inflammatory cytokines, and proliferation and apoptosis of vascular cells through binding to $\alpha 6\beta 1$. In conclusion, our findings indicate that CCN1 is a critical pathophysiological regulator mediating neointima formation induced by complete carotid artery ligation.





Heart rate variability as a prognostic indicator of emotional disorders in patients with mild traumatic brain injury

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Depression and anxiety are the most frequently diagnosed emotional disorders after a mild traumatic brain injury (mTBI); however, predictors of these disorders after an mTBI remain uncertain. Recent research indicated that depression and anxiety are associated with abnormalities in the autonomic nerve system (ANS) which controls heart rate variability (HRV). One analytical algorithm, the frequency-domain analysis of HRV, has gained in popularity with broad applications as a functional index of the ANS. In this study, we investigated whether a power spectrum analysis of HRV can predict the occurrence of emotional disorders such as depression and anxiety in mTBI patients.

The research group consisted of mTBI patients and healthy volunteers from our affiliated hospitals. Two important psychological evaluations, the Beck Depression Inventory (BDI) and Beck Anxiety Inventory (BAI), were used as part of 6- and 12-week follow-up assessments. For both the patient and volunteer groups, we recorded individuals' 5-min resting assessment of HRV. Results showed some significant correlations in serum biomarkers and HRV parameters between healthy volunteers and mTBI patients. The findings also indicated that mTBI patients were vulnerable to emotional disorders, compared to healthy controls, as evaluated by the BAI and BDI scores. In spite of the small sample size, these results also have implications as a potential method for predicting whether mTBI patients are susceptible to emotional disorders using an HRV analysis.





The effect of *Platycodon grandiflorus* on glucose uptake <u>Mei-Jauan Wen (溫美娟)</u> and Shyang-Guang Wang Graduate Institute of Pharmaceutical Science and Technology, Central Taiwan University of Science and Technology

The prevalence of metabolic syndrome has been increasing dramatically due to the sedentary lifestyle and the diet rich in fat and sugar. According to previous research, Saponins isolated from the root of *P. grandiflorus* have showed novel pharmacological effects such as anti-hyperglycemia and anti-lipidemia. It is known when activating insulin receptor (IR), insulin induces signaling pathway through IRS-1 (Insulin receptor substrate 1), PDK (Phosphoinositide-dependent kinase-1), AKT (Protein Kinase B) and then enhancing the uptake of glucose through translocation of GLUT4 vesicles from cytoplasm to the cell membrane. In this study, we demonstrated that *P. grandiflorus* extract induced phosphorylation of IR, IRS-1, PDK, AKT in C₂C₁₂ myotube using the western blotting analysis. In the glucose uptake experiment, *P. grandiflorus* extract improved glucose uptake in cells using ³H-glucose. In addition, the extract also had the beneficial effects on decreasing blood sugar in STZ/nicotinamide-treated mice. In conclusion, *P. grandiflorus* extract could regulate glucose homeostasis in type 2 diabetes.





The extract of Dioscorea opposita determines the effect on regulating blood sugar *in vivo* <u>Chi-Zong Huang (黃啟宗)</u> and Horng-Mo Lee Graduate Institute of Pharmaceutical Science and Technology, Central Taiwan University of Science and Technology

The metabolic syndrome has received a great attention in recent years. The diet with high calories is considered as the risking factors for obesity, hypertension, high triglycerides and hyperglycemia. *Dioscorea opposita* had been reported to have beneficial effects on diabetes in ancient *Chinese pharmacopoeia*. We screened four hundred herbal extracts and found *Dioscorea opposita* extract could improve blood sugar level significantly. The purpose of this study was to investigate how *Dioscorea opposita* to regulate blood sugar. In cell experiments, the phosphorylations of AMP-activated protein kinase (AMPK) and acetyl-CoA carboxylase (ACC) were increased in differentiated C_2C_{12} myotubes that were treated with aqua-extract of *Dioscorea opposita*. In addition, the phosphorylations of Insulin receptor substrate 1 (IRS1), Protein Kinase B (AKT) and S6 kinase 1 (S6K1) were also up-regulated in cells. In animal study, the extract was shown to lower plasma triglyceride level, visceral fat, and weight in the STZ/nicotinamide-induced-diabetic mice fed with high-fat diet. Furthermore, the extract also ameliorated hyperglycemia and improved glucose tolerance in the mice. In conclusion, *Dioscorea opposita* could have beneficial effects on anti-hyperglycemic and anti-obesity.





Roles of spleen tyrosine kinase in IL-17-induced CCL20 chemokine expression in keratinocytes

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Interleukin-17A (IL-17A) is one of the Th17 cytokines and plays an important role in the immunopathogenesis of autoimmune diseases such as psoriasis. Up to date, accumulating evidence has strongly revealed the clinical benefits of inhibition of IL-17A for psoriasis treatment. Syk is a non- receptor tyrosine kinase and has been implicated as a critical mediator in various immune stimulation. Nevertheless, little is known about the relationship of Syk in skin disease and IL-17A signaling. Therefore in this study we used IL-17A-stimulated expression of CC chemokine ligand 20 (CCL20) in normal human epidermal keratinocytes as a cell model to investigate the role of Syk in this aspect. We found that IL-17A stimulation can induce CCL20 gene and protein expression in time- and concentration-dependent manners. Moreover, the activation of IKK, NF-kB, JNK and Syk were observed during IL-17A stimulation. By treating cells with TAK inhibitor and Syk siRNA, we found Syk is an upstream signal molecule of TAK. Inhibition of Syk strikingly attenuated all signal kinases activation and CCL20 secretion induced by IL-17A. Data of promoter activity assay combined with site-directed mutagenesis of CCL20 reporter construct further showed that IL-17A-elicited CCL20 upregulation is depending on Syk-mediated NF-κB pathway. Data using immunoprecipitation also indicated the interaction of Syk with IL-17R downstream signal components such as TRAF6 and Act1 under IL-17A stimulation. However, the essential signaling interaction of TRAF6 and Act1 under IL-17A stimulation was diminished when Syk expression was repressed by siRNA approach. Lastly, using immunocomplex kinase assay we demonstrated that Syk can mediate TRAF6 phosphorylation. Taken together, we for the first time identify Syk as an upstream signaling regulator in IL-17R-mediated Act1-TRAF6 interaction, and demonstrate that Syk plays an essential role for IL-17R-stimulated NF-κB activation and CCL20 gene transcription in primary human keratinocytes. All these findings not only unmask a new role of Syk in IL-17A-mediated inflammatory response, but also shed a new light into the potential therapeutic target of Syk in psoriasis.





Antroquinonol suppresses breast tumor migration/invasion through inhibiting ERK/AP-1- and AKT/NF-кB-dependent MMP-9 and epithelial-mesenchymal transition expressions <u>Wai Theng Lee (李慧婷)</u> and Cheng-Wei Lin Department of Biochemistry, School of Medicine, Taipei Medical University

Antroquinonol (ANQ) is an ubiquinon derivative isolated from *Antrodia camphorata*. However, the effect of ANQ on breast cancer treatment is unknown. We found that ANQ significantly suppressed the migration and invasion of breast cancer MDA-MB-231 cells, and inhibited 12-*O*-tetradecanoylphorbol-13-acetate (TPA)-induced invasiveness by MCF7 cells. ANQ inhibited MMP-9 gene expression and enzymatic activity. Inhibition of ERK and AKT blocked TPA-elicited MMP-9 protein expression, and the addition of ANQ suppressed phosphorylation of ERK and AKT. The induction of the AP-1 and NF-κB pathway participated in MMP-9 transcription. Suppression of ERK inhibited AP-1, whereas blocking AKT diminished NF-κB activity, and treatment with ANQ suppressed both AP-1 and NF-κB signaling. Moreover, ANQ suppressed EMT proteins expression, and inhibited TPA-induced EMT through downregulating the ERK/AP-1 and AKT/NF-κB signaling cascades. Together, our data showed for the first time that ANQ inhibited breast cancer invasiveness by suppressing ERK/AP-1- and AKT/NF-κB-dependent MMP-9 and EMT expressions.





Cooperation of CD49f and IGF-1R signaling in maintenance of pluripotent transcription factor Oct4 of alkaline phosphatase positive mouse germline stem cells

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Introduction : Stem cell niche is known to regulate germline stem cells (GSCs) self-renew and differentiation of germline stem cells (GSCs). Our previously studies has reported that insulin like growing factor 1 receptor (IGF-1R) signaling pathway and CD49f are able to maintain the Oct-4 levels in GSCs. However, the CD49f and IGF-1R downstream regulator that directly regulates the Oct-4 expression in nucleus is still unclear. Hypoxia induce factor 2α (HIF- 2α) known to be induced by hypoxia stress; and the HIF- 2α can bind Oct-4 promoter induce Oct-4 protein expression in nucleus. The aim of this study is to examine whether IGF-1R and CD49f signaling regulate the Oct-4 expression in mouse GSCs through HIF- 2α .

Materials and Methods: CD49f positive mice GSCs were purified by magnetic-activated cell sorting (MACS) and have been confirmed has strong alkaline phosphatase (AP) activity, called CD49f⁺AP⁺GSCs. The GSCs was cultured in laminin-coated plate.

Results: We observed IGF-1 dose-dependently increased the expression of HIF-2 α as well as the Oct-4 in CD49f⁺AP⁺GSC cells. Moreover, experiments using signal inhibitors such as LY2940002 (PI3K inhibitor) and Rapamycin (mTOR inhibitor) effectively suppressed the IGF-1-induced HIF-2 α and Oct-4 expression in GSCs. Meanwhile, we also found out picropodophyllin (PPP, a specific inhibitor of IGF-IR phosphoylation) had lower inhibit ability as well as shIGF-1R so that we suspected there were another signal pathway modulated IGF-1 downstream signal. So we hypothesized CD49f cooperated with IGF-1R on Oct-4 maintenance through PI3K/Akt/mTOR/HIF-2 α in CD49f⁺AP⁺GSC. In our result, inhibition of CD49f by siRNA indicated Akt/mTOR were downregulated. We suppressed CD49f and IGF-1R through transfected siCD49f and shIGF-1R, and discovered HIF-2 α and Oct-4 were restrained obviously.

Conclusion: In our conclusion, CD49f would crosstalk with IGF-1R to regulate Oct-4 expression.







Oridonin inhibits RNA transportation to induce glioma cell apoptosis via down-regulation of RanGAP1 expression <u>Ya-Ling Chang (張雅玲)</u>, Tsung-Yao Lin, Chin-Cheng Lee and Chwen-Ming Shih Graduate Institute of Biomedical Sciences, College of Medicine, Taipei Medical University

Nuclear RanGTP-RNA complex would be hydrolyzed by Ran GTPase activating protein 1 (RanGAP1), and result in the release of RNA into cytoplasm. In this study, 5-30 μ M of oridonin, a natural diterpenoid compound isolated from traditional Chinese medicine *R. rubescens*, induced U87MG glioma cells apoptosis and RNA accumulation in nucleus. After treatment of oridonin, RanGAP1 protein amount was decreased and RanGTP was accumulated in nucleus as investigated using immunoprecipitation and immunofluorescence, respectively, suggesting that down-regulation of RanGAP1 protein level would reduce RNA export via entrapment of RanGTP in nucleus. Over-expression of RanGAP1 protein reversed oridonin-induced U87MG cell death. Hence, we demonstrated for the first time that down-regulation of RanGAP1 protein level by oridonin results in RNA accumulation in nucleus which even lead to cell apoptosis in glioma cells.





Identification gene candidates of kinase downstream signaling regulated by Flavonoid Luteolin in A431-III cells using transcriptome-based analysis

<u>Ru-Long Syu (許如龍)</u> and Chia-Hsiung Cheng Department of Biochemistry, School of Medicine, Taipei Medical University

Flavonoids luteolin is a multiple kinase inhibitor and be used for inhibit tumor cell migration, invasion and angiogenesis. Flavonoids lutrolin and quercetin block EMT transition and NF-kB signaling to inhibit the greater invasion ability of A431-III cells. The kinase signaling regulates downstream gene transcription to affect invasion abilities of tumor cells. Flavonoids are reported as variety of anticancer inhibits, such as cell growth, apoptosis induction, differentiation and kinase inhibition. We reports the transciptiome-based analysis gene transcription treated with Flavonoids luteolin in A431-III cells. Highly transcription changed genes are identified, including up-regulated and down-regulated genes. These genes are the downstream targets of multiple kinases signaling, including Akt, NF-kB, Apoptosis, ribosome biogenesis and metabolic pathway. Some of these genes are reported highly expression in several malignancy tumors and contributes to tumor formation and invasion. Western blot analysis and kinase inhibitors are used to identify the kinase pathways inhibited by luteolin. Collectively, we reports a whole genome genes transcription differentially inhibited by Flavonoids luteolin in A431-III cells to identified downstream target genes. These genes may contribute to highly invasion abilities of A431-III cells and as novel biomarkers for clinical diagnosis and therapeutic targets.





Evaluate Ca2+-r-PGA in wound healing application on human skin cells by ToF-SIMS

Wei-Jhih Lin (林韋誌), Hsiao-Ting Hsieh, Tsui-Yun Lo,

Yu-Ting Lu and Fu-Der Mai

Graduate Institute of Medical Science, Taipei Medical University

Understanding wound healing today involves much more than simply stating that there are three phases: "inflammation, proliferation, and maturation." Wound healing is a complex series of reactions and interactions among cells and "mediators. [1] In this study, calcium form r-PGA (Ca^{2+} -r-PGA) was selected as a mediator agent for wound healing. The r-PGA's physical factors are realty affected by humidity and have high hydrophilic property, excellent water-binding capacity, fine swelling ability and biocompatibility. [2] Through the advantages, during the past decade, r-PGA has been used in suitable for clinical fields. Cellular responses in wound healing cascade are associated with change in the extracellular calcium. In this study, human skin cells (CCD-966SK) were treated with Ca^{2+} -r-PGA. The in vitro biological behavior, cell affinity, as well as, the biodegradability (including cell survival, cell toxicity and cell apoptosis) was evaluated. Besides, the human skin cells of Ca^{2+} -r-PGA has potential efficacy as wound healing material.





財團法人台北市林榮耀教授學術教育基金會 歷年得獎名單

財團法人台北市林榮耀教授學術教育基金會論文獎歷年得獎名冊

第十屆 (102年)

優秀論文獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
林暉皓	國立清華大學生物科技 研究所	江安世	Parallel Neural Pathways Mediate CO2 Avoidance Responses in <i>Drosophila</i>	Science
魏珮琪	國防醫學院生命科學研 究所	李文華	The role of NPGPx in ER stress response	Molecular Cell
白宗彬	國立清華大學生物科技 研究所	江安世	Drosophila ORB protein in two mushroom body-output neurons is necessary for long-term memory formation	Proceedings of the National Academy of the Sciences of the United States of America
林意楝	國立成功大學醫工所	謝清河	Instructive nanofiber scaffolds with VEGF create a microenvironment for arteriogenesis and cardiac repair	Science Translational Medicine
王立傑	長庚大學生物醫學研究 所	張玉生	Interactome-wide analysis identifies end-binding protein 1 as a crucial component for the speck-like particle formation of activated AIM2 inflammasomes	Molecular & Cellular Proteomics

姓名	單位	指导教授	論文題目	學術刊物
王亮傑	國立台灣大學生化科學 研究所	陳宏文	High-temperature requirement protein A4 (HtrA4) suppresses the fusogenic activity of syncytin-1 and promotes trophoblast invasion	Molecular & Cellular Biology
冉毅驊	國立清華大學生物資訊 與結構生物研究所	蕭宏昇	Adenylate kinase-4 is a marker of poor clinical outcomes that promotes metastasis of lung cancer by downregulating the transcription factor ATF3	Cancer Research
劉家宏	國立台灣大學生醫電子 與資訊學研究所	黄奇英	Analysis of Protein-Protein Interactions in Cross-talk Pathways Reveals CRKL Protein as a Novel Prognostic Marker in Hepatocellular Carcinoma	Molecular & Cellular Proteomics
姜寧	國立台灣大學分子與細 胞生物學研究所	王致恬	Cysteine string protein-α regulates fusion pore dynamics during calcium-dependent exocytosis via changing its phosphorylated state	-
周廷蓁	國立成功大學生物化學 暨分子生物學研究所	陳昌熙	Enterohaemorrhagic <i>Escherichia coli</i> O157:H7 Shiga-like toxin 1 is required for full pathogenicity and activation of the p38 mitogen-activated protein kinase pathway in <i>Caenorhabditis elegans</i>	-
施詠馨	國立成功大學藥理學研 究所	王憶卿	Putative Oncogene UBE1C Inhibits the Transcription Activity of p53 in Lung Cancer	-
詹雅衣	國立成功大學藥理學研 究所	陳炳焜	The potential role of ARNT in the regulation of cisplatin- induced cancer cell death	-
陳其欣	國立成功大學藥理學研 究所	王憶卿	Oct4-Mediated Transcriptional Deregulation Promotes Lung Tumor Progression and Drug-Resistance	-





財團法人台北市林榮耀教授學術教育基金會 歷年得獎名單

第九屆 (101年)

優秀論文獎得獎人

姓名	單位	指導教授	論文題目	學術刊物
林士鳴	國立清華大學生物資訊 與結構生物研究所	潘荣隆	Crystal structure of a membrane-embedded H+- translocating pyrophosphatase	Nature 484: 399–403 (2012)
楊文豪	國立陽明大學臨床醫學 研究所	楊慕華	RAC1 activation mediates Twist1-induced cancer cell migration	Nature Cell Biology 14 (4): 366-74 (2012)
潘羿汝	國立中興大學 生命科學系	陳鴻震	FAK is required for assembly of podosome rosettes	Journal of Cell Biology 195: 113-129 (2011)
黄尉倫	陽明大學生化暨分子生 物研究所	王學偉	Snail Regulates Interleukin-8 Expression, Stem-Cell–Like Activity, and Tumorigenicity of Human Colorectal Carcinoma Cells	Gastroenterology 141:279-291 (2011)
黎思宇	國立清華大學生物科技 研究所	江安世	Auditory Circuit in the Drosophila Brain	Proc Natl Acad Sci USA 109: 2607-2612 (2012)

姓名	單位	指導教授	論文題目	學術刊物
林家靖	陽明大學生物化學暨分 子生物研究所	陳志成	An antinociceptive role for Substance P in acid-induced chronic muscle pain	Proc Natl Acad Sci USA 109 (2): E76-83 (2012)
楊盈盈	國立陽明大學公共衛生 研究所	林明薇	Association of the G-protein and alpha-2 adrenergic receptor gene and plasma norepinephrine level with clonidine improvement of effects of diuretics in cirrhotic patients with refractory ascites: a randomized clinical trial	Gut 59: 1545-53 (2010)
楊長青	長庚大學生物醫學所	譚賢明	Epigenetic silencing of myogenic gene program by Myb- binding protein 1a suppresses myogenesis	The EMBO Journal 31, 1739- 1751 (2012)
張慈華	國防醫學院醫學科學研 究所	楊泮池	Slug confers resistance to the epidermal growth factor receptor tyrosine kinase inhibitor	American Journal of Respiratory and Critical Care Medicine 183 (8): 1071-9 (2011)
陳鈺杰	台灣大學分子與細胞生 物學研究所	王致恬	Synaptotagmin III is abundantly expressed in rat retinal neurons to regulate retinal waves during the developmental critical period	-





財團法人台北市林榮耀教授學術教育基金會 歷年得獎名單

第八屆 (100年)

優秀論文獎得獎人

姓名	單位	指導教授	論文題目	學術刊物
劉祐禎	台灣大學生化科學研究 所	李宗璘	Interception of teicoplanin oxidation intermediates yields new antimicrobial scaffolds.	Nature Chemical Biology 7: 304-309 (2011)
吳權娟	生物化學暨分子生物研 究所	詹迺立	Structural Basis of Type II Topoisomerase Inhibition by the Anticancer Drug Etoposide.	Science 333(6041): 459-462 (2011)
林佑憲	國立陽明大學神經科學 研究所	陳儀莊	Dysregulated brain-type creatine kinase is associated withhearing impairment in mice with Huntington's disease.	Journal of Clinical Investigation 121(4): 1519-1523 (2011)
朱自淳	陽明大學神經科學研究 所	陳儀莊	Nuclear translocation of AMPK-a1 potentiates striatal neurodegeneration in Huntington's disease	Journal of Cell Biology 194(2): 209- 227 (2011)
許信賢	陽明大學臨床醫學研究 所	吳國瑞	Bmi 1 is essential in Twistl-induced epithelial-mesenchymal transition	Nature Cell Biology 12(10): 982-992 (2010)

壁報展示獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
吳佩容	國立臺灣大學分子醫學 研究所	陳瑞華	DAPK activates MARK1/2 to regulate microtubule assembly, neuronal differentiation, and tau toxicity	Cell Death and Differentiation 18(9): 1507-1520 (2011)
翁國峰	長庚大學生物醫學研究 所	施信如	Enterovirus 71 3C Protease Cleaves a Novel Target CstF-64 and Inhibits Cellular Polyadenylation	PLos Pathogens 5(9): e1000593 (2009
李松柏	國防醫學院生命科學研 究所所	阮麗蓉	Host-viral effects of chromatin assembly factor 1 interaction with HCMV IE2	Cell Research 21(8): 1230-1247 (2011)
周雅菁	台灣大學醫學院微生物 所	蔡錦華	Requirement for LMP1-induced RON receptor tyrosine kinase in Epstein-Barr virus-mediated B cell proliferation	Blood 118(5): 1340-1349 (2011)
黄鹏年	長庚大學醫學生物研究 所生物技術組	林昭吟	Far Upstream Element Binding Protein 1 Binds the Internal Ribosomal Entry Site of Enterovirus 71 and Enhances Viral Translation and Viral Growth	-

第七屆 (99年)

优秀论文奬得奬人

姓名	單位	指導教授	論文題目	學術刊物
林峰銘	國防醫學院生命科學所	王廷方	Yeast axial-element protein, Red1, binds SUMO chains to promote meiotic interhomologue recombination and chromosome synapsis	EMBO J. 29(3): 586-596 (2010)
周睿鈺	國立陽明大學生命科學 系暨基因體科學研究所	呂俊毅	Multiple molecular mechanisms cause reproductive isolation between three yeast species	Plos Biology 8(7): e1000432 (2010)
呂國昀	陽明大學生理學研究所	李宗玄	Erythropoietin Suppresses the Formation of Macrophage Foam Cells : Role of Liver X Receptor α	Circulation 121: 1828-1837 (2010)

姓名	單位	指导教授	論文題目	學術刊物
李棟樑	中央研究院分子生物研 究所	沈哲鯤	JNK-Mediated Turn-over and Stabilization of the Transcription Factor p45/NF-E2 During Differentiation of Murine Erythroleukemia Cells	Proceedings of the National Academy of Sciences of the United States of America 107 (1): 52-57 (2010)
徐綜遠	台灣大學分子與細胞生 物學研究所	吳益群	Engulfment of Apoptotic Cells in C. elegans Is Mediated by Integrin α /SRC Signaling	Current Biology 20(6): 477-486 (2010)
李國維	國防醫學院生命科學研 究所	余叔美	Coordinated Responses to Oxygen and Sugar Deficiency Allow Rice Seedlings to Tolerate Flooding	Science Signaling 2(91): ra61 (2009)
游成州	台大醫學院生化暨分子 生物學研究所	周綠蘋	Valosin-containing protein plays an important role in the protection of gastric epithelial cells from <i>Helicobacter pylori</i> -induced apoptosis through activation of AKT	-
廖辰芯	長庚大學生物醫學研究 所	林光輝	Dickkopf 4 Positively Regulated by Thyroid Hormone Receptor Suppresses Cell Invasion in Human Hepatoma Cells	-
游舒涵	台大醫學院生化暨分子 生物學研究所	周綠蘋	Phosphoproteomics Approach to Analyze Subcellular Localization Change of Phosphoproteins induced by Helicobacter Pylori	-





財團法人台北市林榮耀教授學術教育基金會 歷年得獎名單

第六屆 (98年)

優秀論文獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
謝幸佳	國防醫學院生命科學研 究所	司徒惠康	Transgenic expression of single-chain anti-CTLA-4 Fv on beta cells protects NOD mice from autoimmune diabetes	Journal of Immunology 183(4): 2277- 85 (2009)
陳立強	長庚大學分子醫學研究 中心	張玉生	Thymidine Phosphorylase is Regulated by hnRNP K-mediated mRNA Stability and is a Prognostic Marker for Nasopharyngeal Carcinoma	Oncogene 28, 1904–1915 (2009);Clinical Cancer Research 14, 3807–3813 (2008)
吳函蒼	陽明大學生物化學暨分 子生物研究所	吳國瑞	Interaction between PHOX2B and CREBBP mediates synergistic activation: mechanistic implications of PHOX2B mutants	Human mutation 30(4): 655-660 (2009)
蔡淑君	台大醫學院微生物研究 所	蔡錦華	EBV Zta protein induces the expression of interleukin-13, promoting the proliferation of EBV-infected B cells and lymphoblastoid cell lines	Blood 114(1): 109-118 (2009)

壁報展示獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
賴琪婷	長庚大學生物醫學研究 所生化分生組	陳華鍵	Study of ebv-mir-BART18-5p targets by proteomics approach	-

第五屆 (97年)

優秀論文獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
李曉暉	台大醫學院生物化學暨分 子生物學研究所	張智芬	Regulation of RhoA-dependent ROCKII activation by Shp2	Journal of Cell Biology 181(6): 999- 1012 (2008)
鄭大山	高雄醫學大學醫學研究 所	洪義人	Glycogen Synthase Kinase 3-beta Interacts with and Phosphorylates the Spindle-associated Protein Astrin	Journal of Biological Chemistry 283(4): 2454-2464 (2008)
陳嘉玲	成功大學基礎醫學研究所	林以行	Ceramide induces p38 MAPK and JNK activation through a mechanism involving a thioredoxin-interacting protein-mediated pathway	Blood 111(8): 4365-4374 (2008)
陳建村	國立陽明大學生化暨分 子生物	魏耀揮	Coordinated Changes of Mitochondrial Biogenesis and Antioxidant Enzymes during Osteogenic Differentiation of Human Mesenchymal Stem Cells	Stem Cells 26(4): 960-968 (2008)

姓名	單位	指導教授	論文題目	學術刊物
陳淑怡	台灣國立中興大學生命科 學系	陳鴻震	Direct interaction of focal adhesion kinase (FAK) with Met is required for FAK to promote hepatocyte growth factor-induced cell invasion	Molecular and Cellular Biology 26(13): 5155-5167 (2006)
黄琤	台大醫學院生化暨分生所	張明富	Large Hepatitis Delta Antigen Is a Novel Clathrin Adaptor-Like Protein	Journal of Virology 81(11): 5985- 5994 (2007)
施景文	陽明大學生化分生所	吳妍華	Candidate tumor suppressor DDX3 RNA helicase specifically represses CAP-dependent translation by acting as an eIF4E inhibitory protein	Oncogene 27: 700-714 (2008)
張心儀	台灣大學分子與細胞生 物學研究所	阮雪芬	Targeting therapy for breast carcinoma by ATP synthase inhibitor aurovertin B	Journal of Proteome Research 7(4): 1433-44 (2008)





財團法人台北市林榮耀教授學術教育基金會 歷年得獎名單

第四屆 (96年)

優秀論文獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
白倩華	陽明大學生物化學所	林俊宏	Dual binding sites for translocation catalysis by Escherichia coli glutathionylspermidine synthetase	The EMBO Journal 25(24): 5970- 5982 (2006)
蔡國旺	國防醫學院生科所	林文昌	Wobble Splicing Reveals the Role of the Branch Point Sequence-to- NAGNAG Region in 3' Tandem Splice Site Selection	Molecular and Cellular Biology 27(16): 5835-5848 (2007)

壁報展示獎得獎人

姓名	單位	指导教授	論文題目	學術刊物
林宜玫	國立成功大學基礎醫學 研究所	孫孝芳	Functional polymorphisms of the human tryptophan hydroxylase 2 genes confer risk for bipolar disorder in Han Chinese	Archives of general psychiatry 64(9): 1015-1024 (2007)
余俊穎	台灣大學分子醫學研究 所	周祖述	A bipartite signal regulates the faithful delivery of apical domain marker podocalyxin/gp135	Molecular Biology of the Cell 18(5): 1710-1722 (2007)
林怡珳	國防生命科學研究所/ 中研院生物醫學研究所	蕭百忍	Partial Duplication at AZFc on the Y Chromosome Is a Risk Factor for Impaired Spermatogenesis in Han Chinese in Taiwan	Human Mutation 28(5): 486-494 (2007)

第三屆 (95年)

優秀論文獎得獎人(博士)

姓名	單位	指導教授	論文題目	學術刊物
林明德	台灣大學分子與細胞生 物學研究所	周子賓	Drosophila decapping protein 1, dDcp1, is a component of the oskar mRNP complex and directs its posterior localization in the oocyte	Developmental Cell 10(5): 601-613 (2006)
趙啟宏	陽明大學生化暨分子生 物研究所	吳妍華	DDX3, a DEAE box RNA helicase with tumor growth-suppressive property and transcriptional regulation activity of the p21 promoter, is a candidate tumor suppressor	Cancer Research 66(13): 6579-6588 (2006)
張元貞	台灣大學生化分生所	張智芬	Contribution of Guanine Exchange Factor H1 in Phorbol Ester- Induced Apoptosis	Cell Death and Differentiation 13(12): 2023-2032 (2006)
徐于喬	陽明大學遺傳所	沈哲鯤	Sumoylation of p45/NF-E2: Nuclear Positioning and Transcriptional Activation of the Mechanism beta-like Globin Gene Locus	Molecular and Cell Biology 25(23): 10365-10378 (2005)

優秀論文獎得獎人(碩士)

姓名	單位	指导教授	論文題目	學術刊物
蔡宏基	台灣大學微生物所	鄧述諄	Involvement of Topoisomerase III in Telomere-Telomere Recombination	Journal of Biological Chemistry 281: 13717-13723 (2006)
許雅涵	台灣大學微生物所	李財坤	Distribution of gyrase and topoisomerase IV on bacterial nucleoid: implication for nucleoid organization	Nucleic Acid Research 34(10): 3128- 3138 (2006)





財團法人台北市林榮耀教授學術教育基金會 歷年得獎名單

第二屆 (94年)

優秀論文獎得獎人(博士)

姓名	單位	指导教授	論文題目	學術刊物
彭瑞銘	台大生化所	梁啟銘	VP1 of Foot-and-Mouth disease virus induces apoptosis via the Akt signaling pathway	Journal of Biological Chemistry 279: 521680174 (2005)
張哲菖	國防生科所	施修明	Daxx mediates the small ubiquitin-like modifier-dependent transcriptional repression of Smad4	Journal of Biological Chemistry 280(11): 10164-73 (2005)
石宗憲	成大基醫所	施桂月	Evidence of human thrombomodulin domain as a novel angiogenic factor	Circulation 111: 1627-36 (2005)

優秀論文獎得獎人(碩士)

姓名	單位	指導教授	論文題目	學術刊物
楊智勝	台大生化所	陳宏文	FBW2 targets GCMa to the ubiquitin-proteasome degradation system	Journal of Biological Chemistry 280(11): 10083-90 (2005)
朱自淳	慈濟神經科學所	楊定一	Protective effects of S-nitrosoglutathione against amyloid b-peptide neurotoxicity	Free Radical Biology and Medicine 38(7): 938-949 (2005)
王郁茜	師大生科系	王憶卿	Wild-type p53 overexpression and its correlation with MDM2 and P14arf alerations: An alternative pathway to non-small cell lung cancer	Journal of Clinical Oncology 23(1): 154-164 (2005)

第一屆 (93年)

優秀論文獎得獎人(博士)

姓名	單位	指导教授	論文題目	學術刊物
詹世鵬	陽明大學微免所	鄭淑珍	The Prp19p-Associated Complex in Spliceosome Activation	Science 302(5643): 279-82. (2003)
許志宏	清華大學分子與細胞生 物所	張大慈	HCMV IE2-mediated inhibition of HAT activity downregulates p53 function	The EMBO Journal 23: 2269-2280 (2004)
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TEMP	37.0c	1	ú	.A	
CO2	5.0%				
RH	90%				
02	21%				
2012-12-31	09:00	Air PIDT:	CO2 CO2	RH RH	02 02

彩色LCD液晶螢幕觸控操作,智慧面板人機互動 滅菌模式操作選擇:145℃乾式滅菌/95℃濕式滅菌 CO2 O2多種氣體運用,數位IR紅外線CO2 O2感測器 高效率過濾網/氣體濾膜ISO Class 5 FDA 認證 低溫培養可選擇原廠內建冷卻循環線圈裝置 機器曾遇斷電再復電時,會提示告知使用者 CO2 O2濃度測定儀/CO2 O2濃度測定液

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TYPE A2	*結構:內部及外部均為不鏽鋼304製,認證NSF/ANSI 49 EN12469
30%排出 70%循環	*機身主體外殼之兩側與背部無烤漆或塗裝材料,為原不銹鋼材製作完成
NU-425 NU-475	* 風扇馬達及UV燈之開關與指示燈,可由控制面板及拉門分別控制啟閉
NU-437 NU-477	*專利設計之袋狀高效率過濾網連結零洩漏氣流系統
NU-440 NU-480	*DC ECM 直流變頻馬達,效率佳、節省能源、最新科技運用
TYPE B1	* 微電腦自動控制風速、彩色LCD液晶螢幕觸控操作
70% 排出 30% 循環	* 數位顯示 Downflow 周速及Exhaust周景

70% 排出 30%循環	*數位顯示 Downflow風速及Exhaust風量
NU-427	*顯示日期、時間、待機、運轉、馬達、UV燈之使用時數
	* 圖樣指示狀態、聲響、視覺及錯誤指示告知,靜音裝置
TYPE B2 100% 排出	* 所有參數資料設定具有密碼鎖定、校正功能
NU-430	* 拉門高度過高或安全櫃內氣流不穩定時,聲響及視覺警告保護操作者
NU-435	*數位氣流感應器,監控濾網承載、電壓與環境因素自動遞補調整風速

動物處理用生物安全櫃 NU-677/NU-629

TYPE A2	*NSF 49 安全認證 * DC ECM直流變頻馬達
30%排出70%循環	* 專利設計高效率過濾網連結零洩漏氣流系統
NU-677	*預濾片補集毛髮皮屑 *活動腳輪或調水平腳選擇
NU-629	* 電動升降調整工作高度,人員或座或站時,舒適操作



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